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us-07-938-154-10.rml

age 1

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 02:38:56 ; Search time 68.15 Seconds  
(without alignments)  
4200.124 Million cell updates/sec

File:  
Prefix score: 1512  
Sequence: 1 ATGCTGCTTCGACGCGGCGG.....CAGCTCCGACCTCCAGCTCA 1512

Scoring table:  
IDENTITY: NUC  
Gapop 10.0 , Gapept 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued.Patents.NA:\*  
2: /cgn2.6/plodata/2/1na/5A.COMB.seq:\*  
3: /cgn2.6/plodata/2/1na/5B.COMB.seq:\*  
4: /cgn2.6/plodata/2/1na/6A.COMB.seq:\*  
5: /cgn2.6/plodata/2/1na/6B.COMB.seq:\*  
6: /cgn2.6/plodata/2/1na/backfile1.seq:\*

Pred. No. is the number of results predicted by search to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1512	100.0	1512	2	US-07-938-154-10
2	1512	100.0	1512	5	PCT-US91-02311-10
3	1162.6	76.9	1521	1	US-08-496-855A-3
4	1162.6	76.9	1521	2	US-07-938-154-9
5	1162.6	76.9	1521	5	PCT-US91-02311-9
6	1159	76.7	2450	2	US-08-466-589-9
7	1159	76.7	2450	3	US-08-700-636-9
8	64159	46.7	2450	3	US-08-467-574-9
9	64159	46.7	1512	1	US-08-466-589-11
10	668.6	45.5	1915	2	US-08-466-589-11
11	668.6	45.5	1915	2	US-08-467-574-11
12	668.6	45.5	1915	2	US-08-700-636-11
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15	452.6	29.9	2377	1	US-08-467-574-1
16	452.6	29.9	2377	1	US-08-700-636-1
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18	452.6	29.9	2377	1	US-08-466-589-5
19	452.6	29.9	2377	1	US-08-466-589-5
20	452.6	29.9	2377	1	US-08-466-589-5
21	360	23.8	1756	2	US-08-700-636-3
22	360	23.8	1756	2	US-08-467-574-3
23	254.6	16.9	1350	3	US-08-462-351-1
24	254.6	16.9	1350	6	519445-2
25	254.6	16.9	1350	6	519445-2
26	254.6	16.9	1350	6	519445-2
27	228.6	15.1	1938	3	US-08-278-635B-1
28	228.6	15.1	1938	3	US-08-464-258B-1

28	228.6	15.1	1938	3	US-08-471-661-1	Sequence 1, Appl 1
29	210	13.9	1876	2	US-08-466-589-7	Sequence 7, Appl 1
30	210	13.9	1876	2	US-08-700-636-7	Sequence 7, Appl 1
31	210	13.9	1876	3	US-08-467-574-7	Sequence 7, Appl 1
32	108	7.1	350	2	US-07-938-154-8	Sequence 8, Appl 1
33	108	7.1	350	5	PCT-US91-02311-8	Sequence 8, Appl 1
34	97.4	6.4	305	2	US-07-938-154-7	Sequence 7, Appl 1
35	97.4	6.4	305	5	PCT-US91-02311-7	Sequence 7, Appl 1
36	77.8	5.1	300	2	US-07-938-154-6	Sequence 6, Appl 1
37	77.8	5.1	300	5	PCT-US91-02311-6	Sequence 6, Appl 1
38	75.2	5.0	209	2	US-07-938-154-2	Sequence 2, Appl 1
39	75.2	5.0	209	5	PCT-US91-02311-2	Sequence 2, Appl 1
40	70.6	4.7	278	5	US-07-938-154-5	Sequence 5, Appl 1
41	70.6	4.7	278	5	PCT-US91-02311-5	Sequence 5, Appl 1
42	70	4.6	250	2	US-07-938-154-4	Sequence 4, Appl 1
43	70	4.6	250	5	PCT-US91-02311-4	Sequence 4, Appl 1
44	64.8	4.3	202	2	US-07-938-154-3	Sequence 3, Appl 1
45	64.8	4.3	202	5	PCT-US91-02311-3	Sequence 3, Appl 1

#### ALIGNMENTS

RESULT 1  
US-07-938-154-10  
Sequence 10, Application US-07-938154  
Patent No. 5981193  
GENERAL INFORMATION:  
APPLICANT: Harpold, Michael M.  
APPLICANT: Ellis, Stephen B.  
APPLICANT: Brust, Paul  
APPLICANT: Akong, Michael  
APPLICANT: Velicelab, Gonul  
TITLE OF INVENTION: HUMAN RECOMBINANT NICOTINIC ACETYLCHOLINE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty Schroeder Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-07-938,154  
FILING DATE: 30-NOV-1992  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA: NO PCT/US91/02311  
APPLICATION NUMBER: R-1991  
PRIORITY APPLICATION DATA: 1991  
APPLICATION NUMBER: US 07/504,455  
FILING DATE: 03-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9380  
TELEPHONE: 619-546-1737  
TELEPHONE: 619-546-1737  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1512 base pairs  
TYPE: nucleic acid  
STANDARDS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:

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Page 2

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NAME/KEY: misc-feature
LOCATION: 1..1512
OTHER INFORMATION: /cds = "Rat neuronal NAcHr beta-2
OTHER INFORMATION: cDNA shown as bottom nucleotide sequence in Figure
OTHER INFORMATION: 9."
LS-07-938-154-10

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Query Match	Similarity	100.0%	Score 1512:	DB 2	Length 1512:
Best Local	Similarity	100.0%	Fred. No. 0:		
Matches 1512:	Conservative	0:	Mismatches	0:	Indels
					Gaps
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Db	1	ATGCGTGGCTTACATGGCGGGCATCTGCACAACTCAATGGCGCTTTGACAGTCAAGCTTCCTT	60		
Oy	61	TGGGTGTGTCAGAGGGGTTTGGGAAATGACACAGAGAGCGGGCTAGTGGAGCATCTCTTA	120		
Db	61	TGGGTGTGTCAGAGGGGTTTGGGAAATGACACAGAGAGCGGGCTAGTGGAGCATCTCTTA	120		
Oy	121	GATCCCTCCCGCTATACAAAGCTGATTTGCTGCACTTCTAAAGCTTCAGCTGGTGACT	180		
Db	121	GATCCCTCCCGCTATACAAAGCTGATTTGCTGCACTTCTAAAGCTTCAGCTGGTGACT	180		
Oy	181	GTAACAGCTATAGTATCATCTGGCTGCACAGCTATAGTGTGCAGAGAGCGGAGCAATATAG	240		
Db	181	GTAACAGCTATAGTATCATCTGGCTGCACAGCTATAGTGTGCAGAGAGCGGAGCAATATAG	240		
Oy	241	ACGACCAATATGCTGGCTGACCCAGAGAGTGGAGAAATACCGGCTCCATCATAGAACCTGAG	300		
Db	241	ACGACCAATATGCTGGCTGACCCAGAGAGTGGAGAAATACCGGCTCCATCATAGAACCTGAG	300		
Oy	301	GACGTGCACATATGAAAGAGTCCGGCTCCCTTCCAAACACATCTGGCTCCCGCAGATG	360		
Db	301	GACGTGCACATATGAAAGAGTCCGGCTCCCTTCCAAACACATCTGGCTCCCGCAGATG	360		
Oy	361	GTTCCTATACAAATGCTAGCGGATGTCGAGAGTCTCTTCTATTCATAGCTGTGGTC	420		
Db	361	GTTCCTATACAAATGCTAGCGGATGTCGAGAGTCTCTTCTATTCATAGCTGTGGTC	420		
Oy	421	TGCTATATGTCAGCATCTTTTGGCTCTACACCGCTCCGCTACGAAGATCATGACAAAT	480		
Db	421	TGCTATATGTCAGCATCTTTTGGCTCTACACCGCTCCGCTACGAAGATCATGACAAAT	480		
Oy	481	GAGGTGAAACATCTCCCATTTTACACAGACGAATTTGCAACATAGATTGGCTCATGAGAC	540		
Db	481	GAGGTGAAACATCTCCCATTTTACACAGACGAATTTGCAACATAGATTGGCTCATGAGAC	540		
Oy	541	TAGACCGTACAGATCACTAGCTGTGTCTACACAGAAATTTGCAACATAGATTGGCTCATGAGAC	600		
Db	541	TAGACCGTACAGATCACTAGCTGTGTCTACACAGAAATTTGCAACATAGATTGGCTCATGAGAC	600		
Oy	601	ACACCCAGCGGGAGTGGAGACATCATGCGACATGCGACAGCGGACGACAGGAGAACCCGAG	660		
Db	601	ACACCCAGCGGGAGTGGAGACATCATGCGACATGCGACAGCGGACGACAGGAGAACCCGAG	660		
Oy	661	GACGTCAAGCTATGTCGAAATCACTGATGATGATGATCAATCTGTGTGCGAAGCAACTGTCTAC	720		
Db	661	GACGTCAAGCTATGTCGAAATCACTGATGATGATGATGATCAATCTGTGTGCGAAGCAACTGTCTAC	720		
Oy	721	ACGTATCAACCTATATCCCTCGGTGACATCATACACGTGGTGGCCATCTGGCTCTCTAC	780		
Db	721	ACGTATCAACCTATATCCCTCGGTGACATCATACACGTGGTGGCCATCTGGCTCTCTAC	780		
Oy	781	CTGGCCCTCAGACTGTGGTGAAGAATGACACTTTTGTATTTTGTGTGTGCTGACACATCAG	840		
Db	781	CTGGCCCTCAGACTGTGGTGAAGAATGACACTTTTGTATTTTGTGTGTGCTGACACATCAG	840		
Oy	841	GTGTTCCGTGCTCATCTATCAGAAATTTGGCTCCCAACCTCTGATGTATGACCGGTGGT	900		
Db	841	GTGTTCCGTGCTCATCTATCAGAAATTTGGCTCCCAACCTCTGATGTATGACCGGTGGT	900		
Oy	901	GCGAAGTACCTATGTTTACCATGTGCTATGACACTTCTCCATGTGACACAGCGTGTGT	960		

Db	901	GGCAAGTACACCAATGGTTTAAACCATGATGTCATGACACCTTCATCTGACACAGCCACACCGCTGTGCA	960
Oy	961	GTCGTGTAATGTCAGACCAACCGCTGCTTACCAAGCAACAGTATGGCCCTGAGTGTACAGTC	1020
Db	961	GTGCTCAATGTGACACCAACCGCTGACCTTACCAAGCAACAGTATGGCCCTGAGTGTACAGTC	1020
Oy	1021	GTCGTGTCGAGAAAGCTGCGCCACACCTGCTCTTCTGTCGACAGCCACACCGCTGTGCA	1080
Db	1021	GTCGTGTCGAGAAAGCTGCGCCACACCTGCTCTGTCGACAGCCACACCGCTGTGCA	1080
Oy	1081	GCTGACCCCTGAGAGCTGTGAGAGCCCGACACGCAACAGTCGAGAGGGCAGGGCTTTCTTC	1140
Db	1081	GCTGACCCCTGAGAGCTGTGAGAGCCCGACACGCAACAGTCGAGAGGGCAGGGCTTTCTTC	1140
Oy	1141	CGTGAAGAGCTCTGGAGGCTTACCCATGTACATCTGCTTTGTCTACACCTGATCAATGCAAGGCG	1200
Db	1141	CGTGAAGAGCTCTGGAGGCTTACCCATGTACATCTGCTTTGTCTACACCTGATCAATGCAAGGCG	1200
Oy	1201	TTGGCTGAGGCGCTTTTCGCAATGACCTACCTGACAGCGCGCGGCGGCGCTGTGAGGCGCA	1260
Db	1201	TTGGCTGAGGCGCTTTTCGCAATGACCTACCTGACAGCGCGCGGCGGCGCTGTGTGGGCGCA	1260
Oy	1261	TGCACGCTGGGCTCCCGGAGACAGTGTGATGGGCTTACGCTTATTTGGGAGACATATGCA	1320
Db	1261	TGCACGCTGGGCTCCCGGAGACAGTGTGATGGGCTTACGCTTATTTGGGAGACATATGCA	1320
Oy	1321	AGTAGAGATGATGACACGAGAGGTGAGGAGACTGGAAATACGTGTGCATGTTGTGAC	1380
Db	1321	AGTAGAGATGATGACACGAGAGGTGAGGAGACTGGAAATACGTGTGCATGTTGTGAC	1380
Oy	1381	GGCGCTGCTCTGTGATCTTTGTCTGTTGTCTGTGTCTTTGGGACCGTGGCATGTTCTTG	1440
Db	1381	GGCGCTGCTCTGTGATCTTTGTCTGTTGTCTGTGTCTTTGGGACCGTGGCATGTTCTTG	1440
Oy	1441	CAGGCTCTCTTCACGAACATACACATGCGCATACCTTCCTCCACCCGACACACTGACGCTCC	1500
Db	1441	CAGGCTCTCTTCACGAACATACACATGCGCATACCTTCCTCCACCCGACACACTGACGCTCC	1500
Oy	1501	AGCTCCCAAGTGA 1512	
Db	1501	AGCTCCCAAGTGA 1512	
RESULT 2			
PCT-US91-02311-10			
Sequence 10, Application PC/TU98102311			
GENERAL INFORMATION:			
APPLICANT: Harpold, Michael M			
APPLICANT: Ellis, Stephen B			
APPLICANT: Akong, Michael			
APPLICANT: Vellicoletti, Gonul			
TITLE OF INVENTION: Human Neuronal Nicotinic Acetylcholine			
TITLE OF INVENTION: Receptor Compositions and Methods Employing Same			
NUMBER OF SEQUENCES: 10			
CORRESPONDENCE ADDRESS:			
SPRINGER, 135 S. LaSalle St.			
CITY: Chicago			
STATE: Ill.			
COUNTRY: USA			
ZIP: 60603			
COMPUTER READABLE FORM:			
MEDIUM TYPE: floppy disk			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: PCT/US91/02311			
FILING DATE: 19910403			
CLASSIFICATION: A35			
ATTORNEY/AGENT INFORMATION			

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NAME: Feder, Scott B  
REFERENCE/DOCKET NUMBER: 51247/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-377-7842  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1512 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
PCT-0591-02311-10

	Query Match Similarity	100.0%;	Score 1512;	DB 5;	Length 1512;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1512;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTGGCTCATGSCGGGCACTCCAAACGACAAATGAGCGCTGTTCAGCTCAGCTTCCTT	60		
DB	1	ATGTGGCTCATGSCGGGCACTCCAAACGACAAATGAGCGCTGTTCAGCTCAGCTTCCTT	60		
QY	61	TGGCTCTCTGACGGGTTTGGGAATGCAACGACAGAGCGGCTATGAGACACCTCTTA	120		
DB	61	TGGCTCTCTGACGGGTTTGGGAATGCAACGACAGAGCGGCTATGAGACACCTCTTA	120		
QY	121	GATCCCTCCGCTATTAACCAAGCTGATTTGGTCACAGCTACTAAAGGGCTCTGAGCTGGAGCT	180		
DB	121	GATCCCTCCGCTATTAACCAAGCTGATTTGGTCACAGCTACTAAAGGGCTCTGAGCTGGAGCT	180		
QY	181	GTACAGCTCATGATATTAATGAGTCAAGCTATTAAGTGTGACAGAGCGGAGACAGATCATG	240		
DB	181	GTACAGCTCATGATATTAATGAGTCAAGCTATTAAGTGTGACAGAGCGGAGACAGATCATG	240		
QY	241	ACGACCATGTCTGGCTGACCCAGAGAGTGGGAATAATTCACGCTCCACATAGAACCTGTAG	300		
DB	241	ACGACCATGTCTGGCTGACCCAGAGAGTGGGAATAATTCACGCTCCACATAGAACCTGTAG	300		
QY	301	GACCTTGACAAATTGAAAGAAAGTCCGGCTCCCTTCGCAAAACACATCTGGCTCCCGAGATGG	360		
DB	301	GACCTTGACAAATTGAAAGAAAGTCCGGCTCCCTTCGCAAAACACATCTGGCTCCCGAGATGG	360		
QY	361	GTCTCTACACAAATCTGACAGCATGTTCGCAAGTCTCTCTTATTCACATGCTGTGTGTC	420		
DB	361	GTCTCTACACAAATCTGACAGCATGTTCGCAAGTCTCTCTTATTCACATGCTGTGTGTC	420		
QY	421	TGCTATGATAGGACAGCATCTTTTGGCTACACAGCTCCGCTACCAAGAGTCATGACAGATTT	480		
DB	421	TGCTATGATAGGACAGCATCTTTTGGCTACACAGCTCCGCTACCAAGAGTCATGACAGATTT	480		
QY	481	GAGGTAAAGCACTTCCCATTTGACACAGCAAGAAATGGACCAATGAAGTTTGGCTATGGAGC	540		
DB	481	GAGGTAAAGCACTTCCCATTTGACACAGCAAGAAATGGACCAATGAAGTTTGGCTATGGAGC	540		
QY	541	TAGACACCTACTGATATTTGACCTGTGTGCTCAAAAGTATGTGGCCAGTCTGGATGATCTC	600		
DB	541	TAGACACCTACTGATATTTGACCTGTGTGCTCAAAAGTATGTGGCCAGTCTGGATGATCTC	600		
QY	601	ACACCCAGGGGAGTGGGAAATCATATGCACTGTGCACAGGCGCAAGCAAGAACCCAGAC	660		
DB	601	ACACCCAGGGGAGTGGGAAATCATATGCACTGTGCACAGGCGCAAGCAAGAACCCAGAC	660		
QY	661	GACTCCACCTGTGTGAGATACACTATTTGACTTATCATTTGCTGCAAAACACACTTCTCTAC	720		
DB	661	GACTCCACCTGTGTGAGATACACTATTTGACTTATCATTTGCTGCAAAACACACTTCTCTAC	720		
QY	721	ACTATCAACCTCATGCTCCTCTGGTACATCATACCTGGCTGGCATCCTCTGGTCTTCTAC	780		
DB	721	ACTATCAACCTCATGCTCCTCTGGTACATCATACCTGGCTGGCATCCTCTGGTCTTCTAC	780		
QY	781	CTGCGCTGAGACGTGTGGGAAGAAGACACTTTGATTTCTGTGCGGTGACACCTAG	840		
DB	781	CTGCGCTGAGACGTGTGGGAAGAAGACACTTTGATTTCTGTGCGGTGACACCTAG	840		

Oy	841	GTGTTGTCGTCGTCATCTCCGAAAGATGAGCTCCGACACCTCGATATGACGGCTGTGT	900
Oy	841	GTGTTGTCGTCGTCATCTCCGAAAGATGAGCTCCGACACCTCGATATGACGGCTGTGT	901
Db	841	GTGTTGTCGTCGTCATCTCCGAAAGATGAGCTCCGACACCTCGATATGACGGCTGTGT	900
Oy	901	GGCAAGACCTCATGTTTACGATGATGCTATGTCACATTCATGCTACACAGCTGTGT	960
Db	901	GGCAAGACCTCATGTTTACGATGATGCTATGTCACATTCATGCTACACAGCTGTGT	960
Oy	961	GTGCTCATGTGTCACACAGCTGTGTACACAGCACATGTGCCCCCTTGAGTGAAGTG	102
Db	961	GTGCTCATGTGTCACACAGCTGTGTACACAGCACATGTGCCCCCTTGAGTGAAGTG	102
Oy	1021	GTCTTCCTGTCGAAAGAGCGCCACCTGCTCTTCGTGACAGCACAGCCACCGCTGTGCA	108
Db	1021	GTCTTCCTGTCGAAAGAGCGCCACCTGCTCTTCGTGACAGCACAGCCACCGCTGTGCA	108
Oy	1081	CGTAGAGCTCTCCGCTTGAGAGAGGAGCGCACACAGAGCTGAGGAGGAGGAGGTTTCTTC	114
Db	1081	CGTAGAGCTCTCCGCTTGAGAGAGGAGCGCACACAGAGCTGAGGAGGAGGAGGTTTCTTC	114
Oy	1141	CGTGAAGGCTCTGGCGCTGACCATGATGACTGCTTTGTCAACCGTCATGATGACAGGCG	120
Db	1141	CGTGAAGGCTCTGGCGCTGACCATGATGACTGCTTTGTCAACCGTCATGATGACAGGCG	120
Oy	1201	TTGGCTGTGGAGGCTTTCGACAGCTGAGCGACATGACGAGCGCGCGCGCTGTGTGGAGCA	126
Db	1201	TTGGCTGTGGAGGCTTTCGACAGCTGAGCGACATGACGAGCGCGCGCGCTGTGTGGAGCA	126
Oy	1261	TGCGAGCTGTGGGCTTCGCGGAAACAGTGGATGGCTGAGCGCTTCATTTGGCGACATATGGA	132
Db	1261	TGCGAGCTGTGGGCTTCGCGGAAACAGTGGATGGCTGAGCGCTTCATTTGGCGACATATGGA	132
Oy	1321	AGTAGAGATGATGACACAGAGTGTGAGGAGAGACTGGAAATAGCTTCCATGTGATGCAC	138
Db	1321	AGTAGAGATGATGACACAGAGTGTGAGGAGAGACTGGAAATAGCTTCCATGTGATGCAC	138
Oy	1381	CGCGTGTCTCTGATCTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	144
Db	1381	CGCGTGTCTCTGATCTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	144
Oy	1441	CAGCGCTCTCTTCGAAAGATGACAGTGCACATGCTTCTCTGACCGCTGACAGCTGACCTCC	150
Db	1441	CAGCGCTCTCTTCGAAAGATGACAGTGCACATGCTTCTCTGACCGCTGACAGCTGACCTCC	150
Oy	1501	AGCTCCAGTAGTA 1512	
Db	1501	AGCTCCAGTAGTA 1512	
RESULT 3			
US-08-496-855A-3			
: Sequence 3, Application US/08496855A			
Patent No. 5801232			
GENERAL INFORMATION:			
APPLICANT: Ellie L. Kathryn J.			
APPLICANT: Ellie L. Kathryn J.			
APPLICANT: Harold Michael M.			
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE			
RECEIVED COMPOSITIONS AND METHODS EMPLOYING SAME			
NUMBER OF SEQUENCES: 6			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Brown, Matlin, Haller & McClain			
STREET: 1660 Union Street			
CITY: San Diego			
STATE: CA			
COUNTRY: U.S.A.			
ZIP: 92101-2976			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.25			

Thu Oct 18 08:54:27 2001

us-07-938-154-10.rni

Page 4

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CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/496,855A
FILING DATE: 20-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/149,503
PRIORITY APPLICATION DATE: 1993
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9369B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0599
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521
TYPE: nucleic acid
STRANDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1521
OTHER INFORMATION: cDNA shown as top nucleotide sequence in
OTHER INFORMATION: Figure...
IS-08-436-855A-3

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Query	Match	Similarity	Score	DB	Length
Query	Match	Similarity	Score	DB	Length
Best Local Similarity	76.9%	Score 1162.6	DB 1	Length 1521	
Matches 118	Conservative	0	Mismatches 194	Indels	Gaps
0					
1	ATGCTGGCTTGCATATGCGCGGCGACACTCAACATCAATGGCGCTGTC	--AGCTTAGCTT	57		
1	ATGCGCGCTGCATGACCGCGGCGTGGTGGTACATACAGACGGCGCTACTGAGACATTC		117		
1	ATGCGCGCTGCATGACCGCGGCGTGGTGGTACATACAGACGGCGCTACTGAGACATTC		117		
58	CTTGGCGCTGCATGACCGCGGCGTGGTGGTACATACAGACGGCGCTACTGAGACATTC		117		
61	CTCGGCTGCTCTCAGGGGTGTGGGTAGCGATACAGAGAGCGCGTGTGGTACATTC		120		
118	TTTGATATCCCTCCGCTATATACAGCTGATATGTCAGTACTAAAGCGCTGTGAGCTGATG		177		
121	CTGATGCTCTTCCGCTACAAAGCTTATCCGCGCCACCAATGGCTGTGAGCTGATG		180		
178	ACTGTACAGCTCATGTATCTATGGCTCAGCTATTAGTGTGCACGAGGGGAGCAGATC		237		
181	ACGTACAGCTTATGTGTGCTACGTGCGCCACGCTCATACAGTGTGAGGGAGACAGATC		240		
238	ATGACACCATCTGCTGCTGCTGACCCAGAGATGGGAATATACGCCCTCAATGAGACCT		297		
241	ATGACACCATCTGCTGCTGCTGACCCAGAGATGGGAATATATGCCCTCAATGAGACCT		300		
298	GAGGATTCGACATATGAGAAAGATCGCGGCTCCCTTCCAAACATCTGGCTCCCGAT		357		
301	GAGGATTCGACATATGAGAAAGATCGCGGCTCCCTTCCAAACATCTGGCTCCCGAT		360		
358	GTCGCTATATCAACATGCTGAGGAGCGATATGACAGTGTCTCTTATTTCCAAATGATG		417		
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421	GTCGCTATATCAACATGCTGAGGAGCGATATGACAGTGTCTCTTATTTCCAAATGATG		477		
478	ATTGAGGATGAGCACTCCATTGTAACACGAGAAATGACATGAAAGTTGCTGCTATG		537		
481	ATTGAGGATGAGCACTCCATTGTAACACGAGAAATGACATGAAAGTTGCTGCTATG		540		
538	ACTGACGACGCTACTGACATGACCTGCTGTCTCAAAAGTATGTGGCCAGTCTGATGAC		597		

Dh	541	ACCTTACGACCGCAGCAGAGATGACCTTGGTGGTGAAGAAGTGAAGGTGGCCAGCGTGGACGAC	600
Qy	598	TTCAACACCGACGGGAGGTGGAGATCATCGCATGCGACGGCCGACGGCAAGCAAGAACCCA	657
Dh	601	TTTCAACACCTAGTGTGTAGTGGAGATCTGGGGCGTGGCGGGAGGCAAGAGAACCC	660
Qy	658	GACGACATCCACTATGTGGAGATACACCTTACATTCATCTTGTGTGGTAAACCACTCTTC	717
Dh	661	GACGACATCTACAGCTGGATGGATACGATGACTTATCTTGTGGCGGCAACCCGCTCTTC	720
Qy	718	TACACTTTCAAACTATCATCTCCCTGGTACTCATCAACGTCGTGGAGCATCTGTGTTC	777
Dh	721	TACACATCAACCTCATCTATCCCTGTGTGCTATCAACCGCTAGCCATCTGTGTCTTC	780
Qy	778	TACGTGCCCTCAACACTGTGGTGAAGAAGATGAACTTTGTATTCTGATCTGTAGACATC	837
Dh	781	TACGTGCCATCTCCAGCTGGGAGGAAGATGAACTGTGTGCAATCTCAAGTCTCTGTGGCGTCC	840
Qy	838	ACGATGTCTGTGCTGTATCTCCAAATTTGTGCTCCACCTCCCTCGATGATACGCTG	897
Dh	841	ACGATGTCTGTGCTGTATCTCCAAATTTGTGCTCCACCTCCCTCGATGATACGCTG	900
Qy	898	GTGGCGAAATCTGTATCTTACGATGTGTGCTACGACCTTTCGATGAGACACAGCG	957
Dh	901	GTGGCGAAATCTGTATCTTACGATGTGTGCTGTGACATCTTTCGATGATACACAGCG	960
Qy	958	TGTGTGTCAAAATGTGACACACCGTGTGCTGTACACAGGACACATGTGGCCCTGTGGTCAAG	1017
Dh	961	TGTGTGTCAAAATGTGACACACCGTGTGCTGTACACAGGACACATGTGGCCCTGTGGTCAAG	1020
Qy	1018	GTGTGTCTTCTGTGGAAGACTCCACCTGCTGTCTTCTGTGAGACGACGACGACGCTGT	1077
Dh	1021	GTGTGTCTTCTGTGGAAGACTCCGCGTGTCTTCTGTGAGACGACGACGACGCTGT	1080
Qy	1078	GCAGCTCAAGCTGTGCTGCTGTGAGAGAGGCCACGAGAGAGCTGTGAGGCG--GAGCGGTT	1134
Dh	1081	GCAGCTCAAGCTGTGCTGCTGTGAGAGAGGCCACGAGAGAGCTGTGAGGCGCGTGTGAGACCTTC	1140
Qy	1135	TTCTTTGCGTGAAGGTCTGTGGGGTGAAGCCATGTATCTGTGTGTGTAACCTCGATCAAGG	1194
Dh	1141	TTCTTTGCGTGAAGCCCGCAGGGGCGGACTCTTTCGACGTGTGCTGTCAACCGGGCGTGGGTG	1200
Qy	1195	CAGGGCTTTGGCTGGGGCTTTTCCAGCTGTGAGGCCACTGCA---GCCGGCCGGGGCGCTGT	1261
Dh	1201	CAGGGGTTTGGCCGGGGCCCTTGGGGGCTGTGGCTGTACCAATGTGGCGGGCCGGGGGCGCTTA	1264
Qy	1252	GTGGGGCATGTGACGTGTGTGCTTCCGGAGACGATGGGCTGTACGCTTCAATTTCGGGAC	1311
Dh	1261	GGGGGAGGTGTGTGTGTGTGCTTCCGGAGACGATGGGCTGTACGCTTCAATTTCGGGAC	1320
Qy	1312	CACATGCGAGTGTGAGATGTGAGGACGACAGCTGTGTGAGGAGGATCGTGAATTTGTGGAC	1371
Dh	1321	CACATGCGGAGGAGGAGATGTGACACGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1380
Qy	1372	GTGATGACGCGCTGTGCTGT	1431
Dh	1381	GTGATGACGCGCTGTGCTGT	1440
Qy	1432	ATGTTCCTGCAAGCTCTTCTTCAGAACTACACTGTGCACTACCTTCTCTCACCTGTAGCAC	1491
Dh	1441	ATGTTCCTGCAAGCTCTTCTTCAGAACTACACTGTGCACTACCTTCTCTCACCTGTAGCAC	1500
Qy	1492	TACAGTCCGACGCTTCCAAATGA	1512
Dh	1501	TACAGCCCGACGCTTCCAAATGA	1521



APPLICANT: Harpold, Michael M.  
 APPLICANT: Ellis, Stephen B.  
 APPLICANT: Brust, Paul  
 APPLICANT: Akong, Michael  
 APPLICANT: Veliclebi, Gonul  
 TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE  
 NUMBER OF SEQUENCES: 12  
 RECEPTOR COMPOSITIONS AND METHODS  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pretty Schroeder Brueggemann & Clark  
 STREET: 444 South Flower Street, Suite 2000  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/938,154  
 FILING DATE: 30-NOV-1992  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US91/02311  
 FILING DATE: 03-APR-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/504,455  
 FILING DATE: 03-APR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reiter, Stephen E.  
 REGISTRATION NUMBER: 31,192  
 REFERENCE/DOCKET NUMBER: 941 9380  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-346-9392  
 TELEFAX: 619-346-4737  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1521 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: misc-feature  
 LOCATION: 1..1521  
 OTHER INFORMATION: /note="Human neuronal NACHr beta-2"  
 OTHER INFORMATION: cDNA shown as top sequence in Fig 9."

Query Match 76.9%; Score 1162.6; DB 2; Length 1521;  
 Best Local Similarity 86.7%; Pred. No. 0;  
 Matches 1318; Conservative 0; Mismatches 194; Indels 9; Gaps 3;

Db 241 ATGACACCAATGCTGGCTGACCCAGAGTGGAGAAATATGCTCCACCTGGAACCT 300  
 298 GAGACCTTCGACATATGAGAAAGTCCGGCTCCCTCCCAAGACATCTGAGCTCCAGAT 357  
 Db 301 GAGAGTTTGGACACATGAGAAAGTCCGGCTCCCTCCCAAGACATCTGAGCTCCAGAT 360  
 358 GTGGTCTATACAAACATGCTGACGGCATGTACGAGTCTCTCTTATTCCAATGCTGTG 417  
 Db 361 GTGGTCTGTCACAAATGCTGACGGCATGTACGAGTCTCTCTTATTCCAATGCTGTG 420  
 418 GTCTCTATGATGACACATCTTGTGCTACCGCATGCTCCATACAGAGTACATGAC 477  
 Db 421 GTCTCTATGATGACACATCTTGTGCTACCGCATGCTCCATACAGAGTACATGAC 480  
 478 ATTGAGTGAAGCACTTCCCATTTGACCGAGAAATTGACCAATGAAAGTTTGCTCATAG 537  
 Db 481 ATTGAGTGAAGCACTTCCCATTTGACCGAGAAATTGACCAATGAAAGTTTGCTCATAG 540  
 538 ACCTAGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597  
 Db 541 ACCTAGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 598 TTACAGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 657  
 Db 601 TTACAGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 658 GAGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 717  
 Db 661 GAGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
 718 TACATACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 777  
 Db 721 TACATACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 778 TACCTGCTCTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837  
 Db 781 TACCTGCTCTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
 838 AGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897  
 Db 841 AGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 898 GTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957  
 Db 901 GTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
 958 TGTGTCTCAATGTGTCACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017  
 Db 961 TGTGTCTCAATGTGTCACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 1018 GTGTCTCTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1077  
 Db 1021 GTGTCTCTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
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 Db 1081 GCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
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 Db 1141 TTTCTCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200  
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 Db 1201 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 1252 GTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1311  
 Db 1261 GTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
 1312 CAGATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1371



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Oy      1252 GGGGAGCCATGACAGCGTGTGGCCTCCGGGAAGCAAGTGATGGCGTAGACGTTGATTGGGAGC   1311
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Db      1261 GGGGAGCCGTTGTGGCTGTGGCCTCCGGGAGCGGTGACGCGCTGCCTTCATTGCCAGAC     1320
Oy      1312 CACATGCGAAGTAGATGATGATGACAGCAAGACTGTGAGGAGAGACTGGAAMTAAGCTTGGCANG   1371
          ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      1321 CACAAGCGGAGCGAGAGCAAGAAGAACCAAGACGTGAAGTGAAGGAACTGAACTACGTGGCAAG   1380
          ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Oy      1432 ATGTTCCTGAGCGCTCTCTCCAGAACTGACATGCACTGCTCTCCAGCAAGCATGGC         1491
          |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
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          |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Oy      1492 TCAGCTCCAGACTCCAAGTGA 1512
          |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      1501 TCAGCCCCAGACTCCAAGTGA 1521
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RESULT 6
US-08-466-589-9
Sequence 9, Application US/08466589
Patent No. 5837489
GENERAL INFORMATION:
Applicant: Eli Lilly & Co., Kathryn J.
Applicant: Eli Lilly & Co., Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTED VISION 1.5
CURRENT PUBLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO.: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2450 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 267..1775
US-08-466-589-9

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Query Match	76.78; Score 1159; DB 2; Length 2450;
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[illegible]

Thu Oct 18 08:54:27 2001

us-07-938-154-10.rni

Page 8

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Db 1285 TGGAGAAAGCTGCCCGCGCGCTTTCATGCACACACCACCGCATCTTTGGCCGCGTAGC 1344
QY 1088 GTCCTCCGCTTGAGAGAGCGCGCCAGCAGAGACGCTGAAGGC--GAGGGGGCTTTCTCGTG 1144
Db 1345 GCGTCCGCGCTGCGGCGACAGCGCCAGCGTACGCGAGAGGCGCTGGAGCGCTTCTTCGCGG 1404
QY 1145 AAGTCTCGCGGCTGACCCCATGTACTGCTTTTTCAAACCTTCATCAATGACAGGCGCTGG 1204
Db 1405 AAGCGCCCAAGCGCGACGACCTGCTCCACATGCGA--GCGGCGCGGCGCGCTTGGAGGTGG 1464
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Db 1465 CCGGGGCGCTTTCGCGGCGTGCAGCTTCACACAGTGGCGCGGCGCTTCAGGGAGCGGT 1524
QY 1262 GCAGCTGTGGCTCCGCGGAAACGAATGATATGGCGGTACGCTTCATTTGGGACACATCGAA 1324
Db 1525 GGTGCTGTGGCGCTCCGCGGAGGCGGTGACGCGGTGCTGCTTCATGTGACACATCGGGA 1584
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QY 1382 GCGCTGTCCGCTGAGATCTTGTCTCTTCTGTCTGTCTTGGACACGTCGGCATTTCTCGC 1441
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QY 1442 ACCGCTGCTTTCGAGAACTACACCTGACCTTCTGCTACACCTGACACATGACATCGCA 1501
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QY 1502 GCTCCAGATGA 1512
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RESULT 7
US-08-700-636-9
Sequence No. 9, Application US/08700636
Patent No. 5910582
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
SPRINGER, 44 S. Selby, Schroeder, Brueggemann & Clark
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,636
FILING DATE: 16-JUL-1996
CLASSIFICATION:
CLASSIFICATION: 536
PRIORITY APPLICATION NUMBER:
PRIORITY DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reller, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 9:

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Page 10

668 CCTATGTGAGACATACCTATGACCTTACATTCCTGCGAAGACACTCTTCTACACTATCA 727  
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CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Halter & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/496,855A  
FILING DATE: 20-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/149,503  
FILING DATE: 08-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/028,031  
FILING DATE: 08-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9369B  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1915 base pairs  
TYPE: nucleic acid  
TOPOLOGY: both  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 87..1583  
US-08-496-855A-5  
Query Match 45.5%; Score 688.6; DB 1; Length 1915;  
Best local similarity 67.4%; Pred No 6,5e-180;  
Matches 1000; Conservative 3; Mismatches 468; Indels 12; Gaps 2;  
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Q	860	CCAAGATGTGCTCTCCCACTCTCTCGATGATACCGCTGTGGGCAAGTACTCATGTTTA	919
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D	1411	ATGAAACCAAGATGTGAGGAGGAGTGGAAATACGTTGGCAATGTATGACACCGCTGT	1470

[illegible]

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RESULT 11
US-08-700-636-11
Sequence 11, Application US/08700636
Patent No. 5910582
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,636
FILING DATE: 16-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1915 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 87..1583
US-08-700-636-11

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	Query Match	Similarity	45.5%	Score 688.6	DB 2	Length 1915
	Best Local	Similarity	67.4%	Pred. 6.5e-180		
	Matches 1000	Conservative	3	Mismatches 468	Indels 12	Gaps 2
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QY	80	TGGGAACATGCACACAGAGAGCGGCTATGTGAGACATCTCTTAAGTCCCTCCGGCTATACAA	139			
Db	151	GGCTGGCCAAATGGCGGAGGAAACATGATGAGACGCTTCTGGAACAAACACCGCTTACATA	210			
QY	140	ACCTGATTTGTCACGCTACTACAGCGCTGTGAGCTGTGACTGTACAGCTCATGTATCAT	139			



Page 13

[illegible]

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1      RESULT 12
2      US-08-467-574-11
3      Sequence 11, Application US/08467574
4      Patent No. 6022704
5      GENERAL INFORMATION:
6      APPLICANT: Eliott, Kathryn J.
7      APPLICANT: Ellis, Steven B.
8      APPLICANT: Harpold, Michael M.
9      TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
10     TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
11     NUMBER OF SEQUENCES: 12
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Brown, Martin, Haller & McClain
14     STREET: 1660 Union Street
15     CITY: San Diego
16     STATE: CA
17     COUNTRY: USA
18     ZIP: 92101-2926
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Diskette
21     COMPUTER: IBM Compatible
22     OPERATING SYSTEM: DOS
23     SOFTWARE: FASTSEQ Version 1.5
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/467,574
26     FILING DATE: June 5, 1995
27     CLASSIFICATION: 536
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 08/028,031
30     FILING DATE: March 8, 1993
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Seidman, Stephanie L.
33     REGISTRATION NUMBER: 33,779
34     REFERENCE/DOCKET NUMBER: 6362-9949
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: 619-238-0999
37     TELEFAX: 619-238-0062
38     TELEX:
39     INFORMATION FOR SEQ ID NO: 11:
40     SEQUENCE CHARACTERISTICS:
41     LENGTH: 1915 base pairs
42     TYPE: nucleic acid
43     STRANDEDNESS: both
44     TOPOLOGY: both
45     MOLECULE TYPE: CDNA
46     FEATURE:
47     NAME/KEY: CDS
48     LOCATION: 87..1583
49     US-08-467-574-11
50
51     Query Match 45.5%; Score 688.6; DB 3; Length 1915;
52     Best Local Similarity 67.4%; Ptd. No. 6.5e-180;
53     Matches 1000; Conservative 3; Mismatches 468; Indels 12; Gaps 2

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 OY 80 TGGGAAGTACAG 139  
 DB 151 GGGTGGCCAAATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 210  
 OY 140 AGCTGATTCGTCAGCTACTAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 199  
 DB 211 ACCCTGATTCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 270  
 OY 200 TGGCTGATTCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 259  
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 OY 320 AAGTCCGCTGCTTCCAAACATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 379  
 DB 391 TCGTGGATTCCTGCAAAAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 450  
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 OY 1154 GGGCTGAG 1207  
 DB 1231 TCTATGAG 1290  
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 DB 1291 GCTTACCGCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1350  
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 DB 1351 AGATGATGAG 1410  
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 DB 1411 ATGATGAG 1470  
 OY 1388 TCGTGGATTCCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1447  
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 DB 1531 TCTTCCAG 1573

RESULT 13  
 US-08-496-855A-1  
 Sequence 1, Application US/08496855A  
 Patent No. 5801232  
 GENERAL INFORMATION:  
 APPLICANT: Eliot, Kathryn J.  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Harpold, Michael M.  
 TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE  
 RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClain  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/496,855A  
 FILING DATE: 20-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/149,503  
 FILING DATE: 08-NOV-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/028,031  
 FILING DATE: 08-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie  
 REGISTRATION/DOCKET NUMBER: 33,779  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0062  
 TELEFAX: 619-238-0062  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2277 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both



Thu Oct 18 08:54:27 2001

us-07-938-154-10.rni

Page 16

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 166..1752
US-08-466-589-1
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RESULT 15
US-08-700-636-1
; Sequence 1, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Eliott, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
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NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELEPHONE: 619-546-4737
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1752
US-08-700-636-1

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Query Match      28.7%; Score 434.6; DB 2; Length 2068;
Best Local Similarity 60.5%; Pred. No. 4,8e-110;
Matches 864; Conservative 0; Mismatches 506; Indels 57; Gaps 7;

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QY 73 GGGGTTTGGGAAGTACAGAGAGAGGAGGAGTGTGAGCATCTTGTGATCCCTCCGCG 132
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Search completed: October 16, 2001, 03:26:25  
Job time: 2849 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 03:00:56 ; Search time 2041.88 Seconds  
(without alignments)  
11453.776 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues  
Total number of hits satisfying chosen parameters: 2688314

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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LOCUS AF145286 1700 bp mRNA ROD 30-MAY-1999
DEFINITION Mus musculus neuronal nicotinic acetylcholine receptor beta 2
ACCESSION AF145286
VERSION AF145286.1 GI:4927272
KEYWORDS
SOURCE
ORGANISM
house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS
Schuetz, U.
TITLE
Cloning of the beta 2 subunit of the mouse neuronal nicotinic
acetylcholine receptor
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1700)
AUTHORS
Schuetz, U.
TITLE
Direct Submission
JOURNAL
Submitted (23-APR-1999) Institut II fuer Anatomie, Universitaet zu
Koeln, Joseph-Stelzmann-Str.9, Koeln 50931, Germany
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LOCUS AR037436
DEFINITION AR037436
ACCESSION AR037436
VERSION AR037436.1 GI:5955292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1521)
AUTHORS Elliott,K.J., Ellis,S.B. and Harpold,M.M.
TITLE DNA and mRNA encoding human neuronal nicotinic acetylcholine
receptor alpha-2 subunit and cells transformed with same
JOURNAL Patent: us 5801232-A 3 01-SEP-1998;
FEATURES
source location/Qualifiers
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BASE COUNT 273 a 499 c 425 g 324 t
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 accession x53179.1 GI:32016  
 version acetylcholine receptor; nicotinic acetylcholine receptor;  
 keywords transmembrane protein.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1. (bases 1 to 1771)  
 AUTHORS Anand, R.  
 JOURNAL Direct Submission  
 submitted (22-MAY-1990) Anand R., The Salk Institute for Biological  
 Studies, P.O.Box 85800, San Diego, CA 92138-9216, USA, The Salk  
 Institute for Biological Studies, P.O.Box 85800, San Diego, CA  
 92138-9216, USA  
 2. (bases 1 to 1771)  
 REFERENCE Anand, R. and Lindstrom, J.

TITLE Nucleotide sequence of the human nicotinic acetylcholine receptor  
 JOURNAL beta 2 subunit gene  
 MEDLINE Nucleic Acids Res. 18 (14), 4272 (1990)  
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RESULT 8

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DEFINITION Human nicotinic acetylcholine receptor beta2 subunit precursor,
mRNA, complete cds.
ACCESSION U62437
VERSION U62437.1 GI:1458121
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2448)
AUTHORS Elliott,K.J., Ellis,S.B., Berckhan,K.J., Urrutia,A.,
Chavez-Noriega,L.E., Johnson,E.C., Velicela,B.G., and Harpold,M.M.
Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits
JOURNAL J. Mol. Neurosci. 7 (3), 217-228 (1996)
MEDLINE 97062879
REFERENCE 2 (bases 1 to 2448)
AUTHORS Elliott,K.J.
JOURNAL Direct Submission
SUBMITTED (28-JUN-1996) Kathryn J. Elliott, SIBIA Neurosciences,
Inc., 505 Coast Blvd. So., La Jolla, CA 92037, USA
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Matches 1312; Conservative 0; Mismatches 190; Indels 9; Gaps 3;
OY 11 GCATGGCGGGGCACTCCAACTCAATGAGCGCTGTC--AGCTTCAAGCTTCTTGGCTGT 67
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 VERSION AR071404.1 GI:7222292  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 UNKNOWN.  
 REFERENCE  
 1 (bases 1 to 2450)  
 AUTHORS Elliott,K.J., Ellis,S.B. and Harpold,M.M.  
 TITLE Human neuronal nicotinic acetylcholine receptor compositions and methods employing same  
 JOURNAL Patent: US 5910582-A 9 08-JUN-1999;  
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VERSION	X53092.1	GI:62957		
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REFERENCE	1 (bases 1 to 1670)			
AUTHORS	Schoeffer, R.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-MAY-1990) Schoeffer R., The Salk Institute for Biological Studies, P.O.Box 85800, San Diego, CA 92138-9216, USA			
REFERENCE	2 (bases 1 to 1670)			
AUTHORS	Schoeffer, R., Whitting, P., Esch, F., Blecher, R., Shlonski, S. and Lindstrom, J.			
TITLE	CDNA clones coding for the structural subunit of a chicken brain			
JOURNAL	nicotinic acetylcholine receptor			
MEDLINE	Neuron 1 (3), 241-248 (1988)			
COMMENT	90166513			
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ACCESSION AF077187  
VERSION AF077187.2 GI:6435834  
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ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 8699)  
Lueders,K.K., Elliott,R.W., Marenholz,I., Mischke,D., Dupree,M. and  
Hamer,D.



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DEFINITION (Acrb2) mRNA, partial cds.
ACCESSION AF089739
VERSION AF089739.1 GI:5531861
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 837)
AUTHORS Lueders,K.K., Elliott,R.W., Marenholz,I., Mischke,D., Dupree,M. and
Hamer,D.
TITLE Genomic organization and mapping of the human and mouse neuronal
beta2-nicotinic acetylcholine receptor genes
JOURNAL Mamm. Genome 10 (9), 900-905 (1999)
MEDLINE 99373254
PUBMED 10441742
REFERENCE 2 (bases 1 to 837)
AUTHORS Lueders,K.K.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1998) Laboratory of Biochemistry, National Cancer
Institute, 37 Convent Dr., Bldg. 37 Rm. 4D14, Bethesda, MD
20892-4255, USA

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BASE COUNT 187 a 252 c 200 g 198 t
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Matches 800; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY 274 GATTACCGCTCTACATGTAAGCCCTGAGGACTTGCACAAATATGAAGAAAGCCGCTCCCT 333
Db 181 GATTATGCCCTCTACATGTAAGCCCTGAGGAGTTTGCACAAATATGAAGAAAGCCGCTCCCT 240

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: Patent No. 5910582  
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: APPLICANT: Eliot, Kathryn J.  
: APPLICANT: Ellis, Steven B.  
: APPLICANT: Harpold, Michael M.  
: TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE  
: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME  
: NUMBER OF SEQUENCES: 12  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
: STREET: 444 South Flower Street, Suite 2000  
: CITY: Los Angeles  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 90071  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/700,636  
: FILING DATE: 16-JUL-1996  
: CLASSIFICATION: 536  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/028,031  
: FILING DATE: 08-MAR-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Reiter, Stephen E.  
: REGISTRATION NUMBER: 31,192  
: REFERENCE/DOCKET NUMBER: P41 9368  
: TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737  
 TELEFAX: 619-546-9392  
 INFORMATION FOR SEQ ID NO: 10:  
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 US-08-700-636-10

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 ; Sequence 10, Application US/08467574  
 ; Patent No. 6022704

## GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.  
 APPLICANT: Ellis, Steven B.  
 APPLICANT: Harpold, Michael M.  
 TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE  
 RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brown, Martin, Haller & McClaim  
 STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92101-2926  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,574  
 FILING DATE: June 5, 1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/028,031  
 FILING DATE: March 8, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L.  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6362-9949  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062  
 INFORMATION FOR SEQ. ID NO.: 10:  
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 MOLECULE TYPE: protein  
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Page 5

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seq documentation block:
; Sequence 6, Application US/08496855A
; Patent No. 5801232
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

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? ADDRESSEE: Brown, Martin, Haller & McClain
? STREET: 1660 Union Street
? CITY: San Diego
? STATE: CA
? COUNTRY: U.S.A.
? ZIP: 92101-2926
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/496,855A
? FILING DATE: 20-JUN-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/149,503
? FILING DATE: 08-NOV-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/028,031
? FILING DATE: 08-MAR-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Seidman, Stephanie
? REGISTRATION NUMBER: 33,779
? REFERENCE/DOCKET NUMBER: 6362-9369B
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619-238-0999
? TELEFAX: 619-238-0062
? INFORMATION FOR SEQ ID NO.: 6:
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? STRANDEDNESS: single
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: Patent No. 5837489
: GENERAL INFORMATION:
: APPLICANT: Elliot, Kathryn J.
: APPLICANT: Ellis, Steven B.
: APPLICANT: Harpold, Michael M.
: TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
: TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Halier & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: CA
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,589
: FILING DATE: June 5, 1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/028,031
: FILING DATE: March 8, 1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 6362-9950
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-238-0999
: TELEFAX: 619-238-0062
: TELEX:
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
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: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
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Ratio: 3.998          Gaps: 4

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Percent Similarity: 82.041 Percent Identity: 63.673

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seq.documentation\_block:  
; Sequence 12, Application US/08700636  
; Patent No. 5910582  
; GENERAL INFORMATION:  
; APPLICANT: Eliot, Kathryn J.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE  
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071



Thu Oct 18 08:54:23 2001

us-07-938-154-10.ra1

age 9

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700.636  
FILING DATE: 16-JUL-1996  
CLASSIFICATION: 536  
PROBATION NUMBER: US 08/028.031  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 498 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-07-938-154-10

Alignment scores:  
Quality: 1607.00 Length: 490  
Ratio: 3.998 Gaps: 4  
Percent Similarity: 82.041 Percent Identity: 63.673

Alignment block:  
US-07-938-154-10 x US-08-700-636-12

Align seg 1/1 to: US-08-700-636-12 from: 1 to: 498

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Thu Oct 18 08:54:23 2001

us-07-938-154-10.rai

Page 10

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seq.documentation_block:
? Sequence 12, Application US/08467574
? Patent No. 6022704
? GENERAL INFORMATION:
? APPLICANT: Elliot, Kathryn J.
? APPLICANT: Ellis, Steven B.
? APPLICANT: Harpold, Michael M.
? TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
? TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
? NUMBER OF SEQUENCES: 12
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Brown, Martin, Haller & McClaim
? STREET: 1660 Union Street
? CITY: San Diego
? STATE: CA
? COUNTRY: USA
? ZIP: 92101-2926
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/467,574
? FILING DATE: June 5, 1995
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/028,031
? FILING DATE: August 9, 1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Seidman, Stephanie L.
? REGISTRATION NUMBER: 33,779
? REFERENCE/DOCKET NUMBER: 6362-9949
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619-238-0999
? TELEFAX: 619-238-0062
? TELEX:
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 498 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? US-08-467-574-12

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seq_name: /cgn2_6/ptodata/2/1aa/7A_COMB.pep:US-08-496-855A-2
seq documentation block:
Sequence 2, Application US/08496855A
Patent No. 5801232
GENERAL INFORMATION:
APPLICANT: Eliott, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,855A
FILING DATE: 20-JUN-1995

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-496-855A-2

alignment_scores:
Quality: 1221.00 Length: 475
Ratio: 3.430 Gaps: 8
Percent Similarity: 74.947 Percent Identity: 51.789

alignment_block:
US-07-938-154-10 x US-08-496-855A-2 ..

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56 Tnrgttrgthguaspargleuphelshtleupne....Argglyty 70
135 TAACAGCTGATTCGCTCAGCTACTAAGCGCTCTGAGCTGAGTGTACTGAC 184
70 rAsnArgTrpAlaArgProValProAsnThrSerAspValAlaIleValA 87
185 ACCTCATGATATCATTTGGCTGCAGCTCATTAGTGTGCACGAGCGGAGCAG 234
87 rghpghlyleuserIleAlaGlnleuIleAspValAspGluIysAsnGln 103
235 ATCATGACACACCAATGCTGTGCTGAGACCGAGAGTGAAGATTACCGCT 284
104 MetMetIthrHisValTrpLeuIysGlnGluTrpSerAspTrpIysLe 120
285 CACATGAGAGCGCTGAGGACTTCGACAAATATGAAGAAGTCCGCTCCCT 334
120 vArgTrpAsnProAlaAspPheGlyAsnIleThrSerLeuArgValPro 137
335 CCAACACATCTGCTGCTCCAGATGTGTTCTATACACATGCTGAGGAG 384
137 erGluMetIleTrpIleProAspIleValLeuTrpAsnAlaIleAspGly 153
385 ARGTCGAAGTCTCTCTTATTCATAGCTGTGCTCTCTTATGATGAGCAG 434
154 GluPheAlaValThrHisMetIhrIysAlaHisLeuPheSerThrIyrH 170
435 CATCTTTGGTACACCTGCTGCATTCACAGAGTGCATGCAAGATTAGG 484
170 rValHisTrpValProProAlaIleTrpIysSerSerIysSerIleAspV 187
485 TGAAGACTTCCCATTTGACAGAGAAATGACCAATGAATGATTGGCTCA 534
187 aThrPhePheProPheAspGlnIleAsnGlyIysMetIysPheGlySer 203
535 TGGACCTAGACCGCTAGTATGATGACCTGTGCTCAAAAGTATGATGGC 584
204 TrpThrIysAspIysAlaIysIleAspLeuGlnGlnMetGlnGlnTrpVa 220
585 CACTGTGATGACTTCACACCGAGGAGTGGAGCATCATCCACTGC 634

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[illegible]

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515 yThr11eGlyLeuPheLeuProPro 523
seq_name: /cgn2_6/ptodata2/laa/6A.COMB.pep:US-08-464-258B-4
seq_documentation_block:
  Sequence 4, Application US/08464258B
  Patent No. 6013766
  GENERAL INFORMATION:
    APPLICANT: ELGOVHEN, ANA BELEN
    APPLICANT: JOHNSON, DAVID S.
    APPLICANT: BOULTER, JAMES R.
    APPLICANT: HEINEMANN, STEPHEN F.
    TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
    TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
    NUMBER OF SEQUENCES: 8
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
      STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
      CITY: SAN DIEGO
      STATE: CALIFORNIA
      COUNTRY: USA
      ZIP: 92121
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/464,258B
      FILING DATE: 06/05/95
      CLASSIFICATION: 530
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/278,635
      FILING DATE: 21-JUL-1994
    ATTORNEY/AGENT INFORMATION:
      NAME: RETTER, STEPHEN E.
      REGISTRATION NUMBER: 31,192
      REFERENCE/DOCKET NUMBER: P41 9989
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 619-677-1409
        TELEFAX: 619-677-1465
      INFORMATION FOR SEQ ID NO: 4:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 511 amino acids
          TYPE: amino acid
          STRANDEDNESS: single
          TOPOLOGY: linear
        US-08-464-258B-4

Alignment_scores:
  Quality: 1205.00      Length: 512
  Ratio: 3.248          Gaps: 11
  Percent Similarity: 72.461  Percent Identity: 47.656

alignment_block:
US-07-938-154-10 x US-08-464-258B-4 ..
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5 Hisser...Alaleuclnphetrprfhlsleutytleutprcysleu 20
64 CTGTGCTAGGGGCTTTG.....GGAATGACACAGAG 97
|||||.....:|||||
20 ulvevalprfoalvalleumrgrnglnclyserhshtrhslalegua 37
98 AGCGGCTAGTGAGCATCTGTAGATCCCTCCGCGCTATACAGCTGATT 147
:::|||||:::|||||:::
37 spbqzleuPheuyshleuPhe.....Glylylylynsaarrgtrpala 51
148 GGTCCACACTACTACGGCTCTGAGCTGTGACCTGACATGTACACCTCAGTATCGATATC 197

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TELEFAX: 619-677-1465  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 510 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-278-635B-4

alignment\_scores:  
Quality: 1202.50 Length: 516  
Ratio: 3.250 Gaps: 12  
Percent Similarity: 71.705 Percent Identity: 47.481

alignment\_block:

US-07-938-154-10 x US-08-278-635B-4

Align seg 1/1 to: US-08-278-635B-4 from: 1 to: 510

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22 CACTCCAACTCAATGGCGCTGTTCAAGCTTCAAGCTTCTTGG..... 63
||||| ..... |||||
5 Hisser...AlaleuclnPhetrprhnlslautylrleutprysleula 20
64 CTGTGCTCAGGGCTTTG.....GGAAGTGAACAAGAG 97
||| ..... |||
20 ulevalrloalvalleuclnphrlnghlserlnlsthlnslaglna 37
||||| ..... |||
98 AGCGGCTAGTGAAGCATCTTAGATCCCTCCGCTATACAAAGCTGATT 147
||||| ..... |||
37 spraglyurphelyshlslaurhe.....gluglyurghasnargtrala 51
||||| ..... |||
148 CGTCCAGCTACTAAGCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTG 197
||||| ..... |||
52 Argrovalrproasnprhserasprvalvallevalrgrheglucse 68
||||| ..... |||
198 ATTGGCTCACTCATATAGTGTGCAGAGGAGGAGGAGGAGGAGGAGG 247
||||| ..... |||
68 flialaglnleuclleasprvalasprclulysanqlmetethrtha 65
248 ATGTCTGGCTGACCCAGAGTGAAGATTCACCGCTCCACATGGAAGCT 297
||||| ..... |||
85 snvalrprleuylsnglnlutrprasnprlyghsnvalargtrprsrro 101
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298 GAGGACTTGACAAATGTAAGAAAGTCCGCTCCCTTCAAAACATGTG 347
||||| ..... |||
102 Alaleuclnphelyshlnvalthrserleuclnphrproserglumetletr 118
||||| ..... |||
348 GCTCCAGATGTGTTCTATACAAAGTGTGAGGAGGAGTGTGAGGAGT 397
||||| ..... |||
118 rlelproasprlevalleuclnphrlnghlserlnlsthlnslaglna 135
||||| ..... |||
398 CTTTCTATTGCAATGCTGTGCTGTCTGTATGATGGCAGCATCTTTGGTA 447
||||| ..... |||
135 hrlhslmetlhrlysalanhlslaurphetrhrglthrvalhnlstrval 151
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448 CCAAGCTCCATGTACAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 497
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152 Protrloalrleuclnphrlnghlserlnlsthlnslaglna 168
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498 ATTGTCAGGAGAAATGTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 547
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168 orphelarglnghlserlnlsthlnslaglna 185
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548 GTATGAGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 597
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185 ysatalyslslasprleuclnphrlnghlserlnlsthlnslaglna 601
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598 TTCAACAGCCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 647
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235 yrphelvalleargarglaurleuclnphrlnghlserlnlsthlnslag 251
||||| ..... |||
739 CCGTCCAGCTCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 788
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252 Proclslleuclnphrlnghlserlnlsthlnslaglna 268
||||| ..... |||
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||||| ..... |||
268 rclucsglglulyslthrleuclnphrlnghlserlnlsthlnslaglna 285
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285 hrvalrphelrleuclnphrlnghlserlnlsthlnslaglna 301
||||| ..... |||
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||||| ..... |||
302 llerphelrleuclnphrlnghlserlnlsthlnslaglna 318
||||| ..... |||
939 CTCCATGCTCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 988
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1039 CCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1073
||||| ..... |||
352 Proalrgrlreulmetlasmrgrlroleuclnphrlnghlserlnlsthln 368
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1093 .....CGTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1128
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385 etaspralaglnluthrghlserlnlsthlnslaglna 401
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||||| ..... |||
402 Asnle.....cysvalcysalael 408
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408 ylerprroasprsermercllyvalleuclnphrlnghlserlnlsthln 425
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1214 TCCGAGT...GAGCCACTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1251
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||||| ..... |||
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seq\_name: /cgn2\_6/plodata/2/lae/6a\_comb\_rep:us-08-471-961-4

seq\_documentation\_block:

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: Sequence 4, Application US/08471961
: Patent No. 6100046
: GENERAL INFORMATION:
:   APPLICANT: ELGOYHEN, ANA BELEN
:   APPLICANT: JOHNSON, DAVID S.
:   APPLICANT: BOULDER, JAMES R.
:   APPLICANT: HEINEMANN, STEPHEN F.
:   TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
:   NUMBER OF SEQUENCES: 8
:   CORRESPONDENCE ADDRESS:
:   ADDRESS: GRAY CARY WARE & FREDENRICH
:   STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
:   CITY: SAN DIEGO
:   STATE: CALIFORNIA
:   COUNTRY: USA
:   ZIP: 92121
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: FLOPPY disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/471,961
:   FILING DATE:
:   CLASSIFICATION:
:   PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 08/278,635
:   FILING DATE: 21-JUL-1994
:   ATTORNEY/AGENT INFORMATION:
:   NAME: REITER, STEPHEN E.
:   REGISTRATION NUMBER: 31,192
:   REFERENCE/DOCKET NUMBER: P41 9771
:   TELEPHONE: 619-677-1409
:   TELEFAX: 619-677-1465
:   INFORMATION FOR SEQ ID NO: 4:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 510 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:   US-07-938-154-10 x US-08-471-961-4

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alignment\_scores:                      Quality: 1202.50                      Length: 516  
    Ratio: 3.250    Gaps: 12  
    Percent Similarity: 71.705                      Percent Identity: 47.481

alignment\_block:  
 US-07-938-154-10 x US-08-471-961-4 ..

Align seg 1/1 to: US-08-471-961-4 from: 1 to: 510

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5 HisSer...AlaLeuclnPhetrprhrlhslLeuTyrLeuTprCysLeu 20
64 .CTGTCTCAGGGGTTTGG.....GGACTGACACAGAG 97
20 uleuValProAlaValleuThrGlnGlnIysSerhlsThrhlslalaGlu 37
98 AGCGGCTAGTGAAGCATCTTCATGATCCCTCCGCTATACAAGGATTT 147
37 sprArgleuPhelYshlsLeuPhe.....GlyGlyTyrIasnArgTrpala 51
148 CGTCCAGCTCAATGAGGCTCTGAGCTGAGTGAAGTCAAGTCAATGATG 197
52 AtrpValAlaProasnThrSerAspValValIleValAlaPheGlyLeuSe 68
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68 rleAlaGlnleuIleAspValAspGluYasnGlnIleMetThrTrpA 85
248 ATGTCGGCTGACCCAGAGTGGAGATTTACCGCTTCATGAGAGCT 297
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102 AlaGlnPheGlyAsnValThrSerleuArgValProSerGlnMetLeuTr 118
348 GCTCCAGATGCTTCTATACAAATGCTGACGAGCATGATGAGAGTCT 397
118 pIleProAspIleValleuTyrIasnAsnAlaAspGluPheAlaValTr 135
398 CTTTCTATTCCAAATGCTGCTCTCTATGATGACGACATCTTTGGCTA 447
135 hrhlsMetThrIysAlaAlaIlePhePheThrGlyThrValhlsTrpVal 151
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152 ProProAlaIleTyrIysSerSerIleAspValThrPhePheTr 168
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185 YsAlaIysIleAspLeuGlnGlnIleGluArgThrValAspLeuYsAsp 201
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689 ACTTCATCATTCGTCGCGAACAACACTCTTCATCACTATCAACCTCATG 738
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739 CCTGCGTACTCATCACCTGCGTGGCCATCTGCTTACCTGCCCTC 788
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789 AGACTGTGTGAAGATGACACTTGTATTTCTGTGCTGAGTCACTCA 838
268 rGluCysGlyGluIleThrIleuYsIleSerValleuLeuSerleuTr 285
839 CGGTGTCCTGCTGCTCATCTCCAAAGATGTGCTCCACCTCCCTCAT 888
285 hrValPheleuIleuIleThrGlnIleleProSerThrSerleuVal 301
889 GTACCGCTGTGGGCAAGTCACTCATGTTTACCATGGTGTACTACCTT 938
302 IleProleuIleGlyGluYrleuIleuPheThrMetIlePheValThrle 318
939 CTTCATGCTCAACGAGCTGTGTGCTGCATGTGCACACCGCTGCCGCA 988
318 uSerIleValIleThrValPheValIleuAsnValhlsIasnArgSerPro 335
989 CACAGCACACCATGCCCCCTGGGTCAAGGTGCTTCTGTGGAAGAGCTG 1038
335 eThrIleAsnMetProAsnTrpValArgValAlaIleuLeuGlyArgVal 351
1039 CCGACCGCTGCTCTCCGTCGACGAGCA.....CGCACCG 1073
352 ProArgTrpIleuMetIleAsnArgProleuProPheGlnIleuIlehls 368
1074 CTGTGACAGCTCAGCGTCTG..... 1092

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368 ySerProAspLeuLysLeuSerProSerTyrHisTrpLeuGluTrpAsn 385
1093 .....CGCTTGAGGAGCGCCAGAGAGCGGTAGGGCGAG 1128
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385 eLAspAlaGluArgGluGluThrGluGluGluGluGluGlu 401
1129 GCGGTTTTCGCTGAAGTCTCTGGCGGTGACCCATGTACTGCTTGT 1178
      :::::   |||   |||
402 AsnIle.....CysValCysAlaGlu 408
1179 CAACCTGCAATGATGACGAGCGCTTGCGTGGGCT.....T 1213
      |||   |||   :::::   :::::
408 yLeuProAspSerSerMetGlyValLeuTyrGluHisGlyLeuHisL 425
1214 TCGGAGCT...GAGCCACATGCGCCGCGCGCGGCGCTCT..... 1251
      ::|||   |||   :::::   |||
425 euAlaGluMetGluProGluThrGluThrProSerGluHisLeuGlu 441
1252 ...GTGGGGCCATGCAGCTGTGCGCTCCGGGAAGCAGTGAGTGGCTACG 1298
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442 LeuLeuSerPro.....GluIleGluLysAlaLeuGluGluValHis 455
1299 CTTCATTCGCGACACATGCGAGAGTAGATGATGACACAGAGTGTAGAG 1348
      :::::   |||   :::::   |||
455 sTyrIleAlaAspArgLeuArgSerGluAspAlaSerSerValLysG 472
1349 AGACGTGGAATACGTGGCCATGATGACGCGCTGTCTCTGTGATGATG 1398
      |||   |||   |||   |||   |||   |||   |||   |||
472 LuAspTrpLysTyrValAlaMetValAlaAspArgLLeuLeuTrpLeu 488
1399 TTGTCTTTGTCTGTCTTTGGGACCGTGGCATGTTCTGACGCT 1446
      |||   |||   ::|||   ::|||   ::|||   ::|||   |||
489 PheIleIleValLysPheLeuGlyThrIleGlyLeuPheLeuProPro 504

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seq documentation block:
? Sequence 5, Application US/08278635B
? Patent No. 5683912
? GENERAL INFORMATION:
? APPLICANT: ELGOYHEN, ANA BELEN
? APPLICANT: JOHNSON, DAVID S.
? APPLICANT: BOULTER, JAMES R.
? APPLICANT: HEINEMANN, STEPHEN F.
? TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: GRAY CARY WARE & FRIEDENRICH
? STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
? CITY: SAN DIEGO
? STATE: CALIFORNIA
? COUNTRY: USA
? ZIP: 92121
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/278.635B
? FILING DATE: 21-JUL-1994
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: REITER, STEPHEN E.
? REGISTRATION NUMBER: 31,192
? REFERENCE/DOCKET NUMBER: P41 9771
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619-677-1409
? TELEFAX: 619-677-1465
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 497 amino acids

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? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-278-635B-5

alignment_scores:
      Quality: 1193.50      Length: 508
      Ratio: 3.200      Gaps: 9
      Percent Similarity: 73.425      Percent Identity: 46.850

alignment_block:
US-07-938-154-10 x US-08-278-635B-5 ..

Align seg 1/1 to: US-08-278-635B-5 from: 1 to: 497

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2 GlyValValLeuLeuProProProLeuSerMetLeuValLeu 18
82 .....GGACTGACAGAGAGAGCGGCTGATGAGCATCTC 117
18 etLeuLeuProAlaAlaSerGluAlaGluHisArgLeuPheGluTrpLeu 34
118 TTGATTCCTCCCGCTATACAGCTGATGCTGCAGCTACTACGCTC 167
35 PheGluAsp....TyrAsnGluIleLeuArgProValAlaAsnValSe 49
168 TGAGTGTGACTGTACAGCTCATGATGATCATTTGCTGAGCTCAATG 217
49 rHisProValIleIleGluPheGluValSerMetSerGluLeuValLysV 66
218 TGACAGCGGGGAGAGATCATGACACCAATGCTGCGTGCACCGAGAG 267
66 alAspLysValAlaSerGluIleMetGluThrAsnLeuTrpLeuLysGluIle 82
268 TGGGAAGATTACCGCTCACAATGAGAGCTGAGACTTGCAATATGAA 317
83 TrpAsnAspTyrLysLeuLysTrpLysProSerAspTyrGlnGlyValG 99
318 GAAGTCCGCGCTCCCTCCAAACACATCTGGCTCCAGATGCTGTCTAT 367
99 uPheMetArgValProAlaGluLysLLeuTrpLysProAspLysLeuVal 116
368 ACAACAATGCTGAGCGCATGATGAGAGTCTGCTATATCAAGTGTG 417
116 yTrAsnAsnAlaAspGlyAspPheGluValAspAspLysThrLysAlaLeu 132
418 GTCTCTATGATGAGCAGCATCTTTGGCTACCACTGCAATTCACAAAG 467
133 LeuLysTyrThrGlyValValThrTrpIleProProAlaIlePheLysSe 149
468 TGCATGCAAGATTGAGGTGAGCACTTCCCATTTGACCAAGCATGCA 517
149 rSerCysLysIleAspValThrTyrPheProPheAspTyrGlnAsnGly 166
518 CCAATGAGTTGGCTACAGCACTGACAGCCGACTGAGAAATGAGCTG 567
166 rMetLysPheGlySerTrpSerTyrAspLysAlaLysIleAspLeuVal 182
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183 LeuIleGlySerSerMetAsnLeuLysAspTyrTrpGlnSerGlyLys 199
618 GAGCATGATGCGACTGCGCGAGCGGCAAGAG.....AAACGAG 658
199 palAlaIleLysAlaProGlyTyrLysHisGluLysLysTyrAsnGly 216
659 AGCACTCACCTATGTGAGCATCACTTGAATTCATCATTCGTCGAAA 708
216 ySerGluLysIleTyrGlnAspIleThrTyrSerLeuTyrIleArgArgLeu 232
709 CCACCTCTACACTATCAACCTCATCCCTGCGTACATCACTACCTC 758

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  Patent No. 6100046
  GENERAL INFORMATION:
  APPLICANT: EICOWHEN, ANA BELEN
  APPLICANT: JOHNSON, DAVID S.
  APPLICANT: BOULDER, JAMES R.
  APPLICANT: HEINEMANN, STEPHEN F.
  TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
  NUMBER OF SEQUENCES: 8
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: GRAY CARY WARE & FREIDENRICH
  STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
  CITY: SAN DIEGO
  STATE: CALIFORNIA
  COUNTRY: USA
  ZIP: 92121
  COMPUTER READABLE FORM:
  MEDIUM TYPE: floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, version #1.25
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/471,961
  FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/278,635
  FILING DATE: 21-JUL-1994
  ATTORNEY/AGENT INFORMATION:
  NAME: REITER, STEPHEN E.
  REGISTRATION NUMBER: 31,192
  REFERENCE/DOCKET NUMBER: P41 9771
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 619-677-1465
  TELEFAX: 619-677-1465
  INFORMATION FOR SEQ. ID NO: 5:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 497 amino acids
  TYPE: amino acid

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OM of: US-07-938-154-10 to: A.Geneseq\_0601.\* out-format : pfs

Date: Oct 16, 2001 6:00 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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-O=/cgml\_1/USPRO.spool/5981193/runat\_15102001\_132923\_21306/app-query.fasta.1.1596  
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000  
-GAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
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-TRANS-human40.cdt -LIST=45 -DOCALIGN=200 -THR=SCORE=pct  
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# Search information block:

Query: US-07-938-154-10  
Query length: 1512  
Database: A.Geneseq\_0601.\*  
Database sequences: 412676  
Database length: 60623986  
Search time (sec): 64.420000

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DT	14-MAY-1998	(first entry)		
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DE	Human neuronal nicotinic acetylcholine receptor beta-2 subunit.			
XX				
KW	Human; neuronal nicotinic acetylcholine receptor; beta-2 subunit;			
XX	brain tissue; screening; NACHR; antibody.			
OS	Homo sapiens.			
XX				
FT	Key	Location/Qualifiers		
FT	Peptide	1..25		
FT	Domain	/label= signal		
FT	Domain	234..259		
FT	Domain	/label= TMD1		
FT	Domain	/note= "transmembrane domain"		
FT	Domain	267..288		
FT	Domain	/label= TMD2		
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FT	Domain	295..320		
FT	Domain	/label= TMD3		
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FT	Domain	453..477		
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FT	Region	/label= cytoplasmic_loop		
PD	WO9420617-A2.			
XX	15-SEP-1994.			
XX	08-MAR-1994.	94WO-US02447.		
XX	08-MAR-1993.	930S-0028031.		
XX	(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.			
XX	(SIBT-) SIBIA NEUROSCIENCES INC.			
XX	Elliot KU, Ellis SB, Harpold MM;			
XX	WPI; 1994-303024/37.			
XX	N-PSDB; AAV12201.			
PT	Human neuronal nicotinic acetylcholine receptor subunits and DNA -			
PT	also transformed cells useful for screening cpds. which modulate			
PT	activity of the receptor			
XX	Example 2; Page 84-85; 99pp: English.			
XX				
XX	The present sequence represents a human neuronal nicotinic acetylcholine			
XX	receptor (NACHR) subunit. The cells expressing the alpha and/or beta			
XX	NACHR subunits may be used in a method of screening compounds to			
XX	identify any which modulate the activity of human neuronal NACHR.			
XX	Subunit specific antibodies may be used to monitor the distribution			
XX	and expression density of various subunits in normal vs diseased brain			
XX	tissues. Testing of single receptor subunits or specific receptor			
XX	subunit combinations with a variety of potential agonists or antagonists			
XX	provides information with respect to the function and activity of the			
XX	individual subunits and should lead to the identification and design of			
XX	compounds that are capable of very specific interaction with one or			
XX	more receptor subtypes. The resulting drugs should exhibit fewer			

CC unwanted side effects than drugs identified e.g. screening with cells  
CC that express a variety of subtypes.

50 Sequence 502 AA:

alignment\_scores:

Quality: 2432.00 Length: 492  
Ratio: 5.067 Gaps: 2  
Percent Similarity: 97.561 Percent Identity: 94.106

alignment\_block:

US-07-938-154-10 x AAM44157 ..

Align seg 1/1 to: AAM44157 from: 1 to: 502

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seq\_documentation\_block:

ID AAW09026 standard; Protein: 502 AA.

AC AAW09026;

DT 09-APR-1997 (first entry)

DE Neuronal nicotinic acetylcholine receptor beta-2 subunit.

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KM      Ligand-gated receptor.
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OS      Homo sapiens.
XX      MO9641876-A1.
XX      PD
XX      27-DEC-1996.
XX      PE
XX      07-JUN-1996; 96MO-US09775.
XX      PR
XX      07-JUN-1995; 95US-0484722.
XX      PA
XX      (SIBI-) SIBIA NEUROSCIENCES INC.
XX      PI
XX      Elliott KJ, Harpold MW;
XX      WPI: 1997-065463/06.
XX      DR
XX      N-PSDB; AAT48240.
XX
XX      Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
XX      used in screening to determine the effect of drugs on the receptor
XX      Disclosure; Page 77-78; 108pp; English.
XX
XX      The beta-2 subunit (AAW09026) of the human neuronal nicotinic
XX      acetylcholine receptor (nAChR) can be expressed in transformed
XX      host cells carrying beta-2 subunit DNA (see also AAT48240). Host
XX      cells, esp. mammalian cells or amphibian oocytes, expressing the
XX      recombinant beta-2 subunit, opt. in combination with other
XX      recombinant alpha and/or beta subunits (see also AAW09018-25,
XX      AAW09027), can be used to examine the function of human AChR and
XX      to identify cpds. that modulate its activity.
XX
XX      Sequence 502 AA:
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XX      27 pThrGluGluAlaGlyLeuValGluHisLeuLeuAspProSerArgTyrAsnL 44
XX      140 AGCTGATTGCTCAGCTACTAAAGGCTGTGAGCTGAGCTGACTATACAGCTC 189
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XX      190 ATGCTGTCATTTGGCTCAGCTACTATAGTGTGACAGAGCGGAGCGAGATCAT 239
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XX      240 GACCAACAATGTCTGCTGACCCAGAGAGTGGAGATTACCGCTACAT 289
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XX      77 tThrThrAsnValTrpLeuThrGlnGluTrpGluAspTyrArgLeuThr 94
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540 CTACGACCTGACTGAGATTGACCTGGTGCCTCAAAAGATGATGTGCGAGTGC 589
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590 TGGATGACTTCACACCCAGCGGAGAGTGGAGACATCATGTGCGACAGC 639
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940 TGCATGCTCAGCAGCGTGTGTGTGTCATGTGACACACCGCTCCGCTTAC 989
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 1334 ACCAGAGTGTGAGGAGACATGGAATACGTTGACATGGTATGACGCCG 1383  
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 461 LeuPheLeuTrpIlePheValIlePheValIlePheGlyThrIleGlyMe 477  
 1434 CTTCCTGACGCTCTCTTCACAGACATACACCTGCACTACCTTCCTCCAC 1483  
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 DT 09-APR-1997 (first entry)  
 DE Neuronal nicotinic acetylcholine receptor beta-4 subunit.  
 XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;  
 KM ligand-gated receptor.  
 XX Homo sapiens.  
 OS  
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 PD 27-DEC-1996.  
 PF 07-JUN-1996; 96WO-US09775.  
 PR 07-JUN-1995; 95US-0484722.  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 PI Ellloft KJ, Harpold MM;  
 DR WP1: 1997-065463/06.  
 DR N-PSDB: AAT48241.  
 PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -  
 XX used in screening to determine the effect of drugs on the receptor  
 XX Disclosure: Page 85-86; 108pp; English.  
 CC The beta-4 subunit (AAW09026) of the human neuronal nicotinic  
 CC acetylcholine receptor (nAChR) can be expressed in transformed  
 CC host cells carrying beta-4 subunit DNA (see also AAT48241). Host  
 CC cells, esp. mammalian cells or amphibian oocytes, expressing the  
 CC recombinant beta-4 subunit, opt. in combination with other  
 CC recombinant alpha and/or beta subunits (see also AAW09018-26), can  
 CC be used to examine the function of human AChR and to identify cpds.  
 CC that modulate its activity.  
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 Gaps: 4

Percent Similarity: 82.653 Percent Identity: 64.490

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 81 GGAAGTGCACAGAGAGAGCGGCTAGTGAGCATCTTAATCCCTCC 130  
 22 gValAlaAsnAlaGluGluLysLeuMetAspAspLeuLeuAsnLysTrpA 39  
 131 GCATTAACAAGCTGATTCGTCAGCTACTAACGGCTCGAGCTGGTGACT 180  
 39 rGlyAsnAsnLeuIleArgProAlaIrrSerSerSerGlnLeuIleSer 55  
 181 GTACACCTCATGTATTCATTCGCTCAGCTCATTAAGTTCAGCAGCGGGA 230  
 56 IleLysLeuGlnLeuSerLeuAlaGlnLeuIleSerValAsnGluArgL 72  
 231 GCAGATCATGACCCACCATGTCTGCTGACCCAGAGGTGGAGATTAC 280  
 72 uGlnIleMetThrThrAsnValTrpLeuLysGlnGluTrpThrAspTrpA 89  
 281 GCCTCATGAGAAGCTGAGAGACTTCAGCAATATGAGAAGAAGTCGGCTC 330  
 89 rGluThrTrpAsnSerSerArgTrpGluGlyValAlaAsnIleLeuAlaG 105  
 331 CCTTCCAAACATCTGGCTCCAGATGCTGTCTATACACATAGCTGA 380  
 106 ProAlaLysArgIleTrpLeuProAspIleValLeuTrpAsnAsnAlaAs 122  
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XX
KW Rat; nAChR.
XX
OS Rattus rattus.
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FH
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FT Cleavage-site 20..21 /label=signal peptide
FT 21..495 /note=membrane spanning region**
FT 237..256 /label=membrane spanning region**
FT 257..285 /label=MSR I
FT 286..318 /label=MSR II
FT 319..338 /label=MSR III
FT 339..348 /label=MSR IV
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FT 366..385 /label=MSR VI
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XX      14-MAR-1989; 89US-0321384.
XX
XX      (SALK ) SALK INST FOR BIOL STUD.
XX
XX      Heinemann SF, Deneris ES, Duvolsin RM, Patrick JW;
XX      WPI; 1990-304987/40.
XX      DR
XX      N-PSDB; AAQ06068.
XX
XX      New neuronal nicotinic acetylcholine receptor - compans. contg.
XX      beta 4 sub-unit and DNA sequences encoding them.
XX
XX      Claim 8; Fig 3; 47pp; English.
XX
XX      The sequence of a novel neuronal nicotinic acetylcholine
XX      receptor subunit beta 4 was deduced from cDNA obtd from pPRC13
XX      (ATCC 67893) isolated from a cDNA library in lambda ZAP II prep.
XX      from rat mRNA. The protein subunit can combine with the known
XX      subunits , alpha-2, -3, and -4, and beta-2 to form previously
XX      unknown functional receptors. The new subunit is expressed in
XX      the central and peripheral nervous systems and in PC12 cells.
XX      It has the characteristics of a ligand-gated ion channel subunit,
XX      including four transmembrane domains. The cystein residues 128
XX      and 142 of the Torpedo electric organ alpha subunit are present
XX      at posns. 152 and 166. The beta 4 subunit is distinctive in
XX      having four rather than two glycosylation sites. Of the three
XX      neuronal beta-type subunits, beta 4 has the largest cytoplasmic
XX      domain.
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588 TCTGGATGACTTCAACCAAGCGGAGTGGAGCATCATCGACATGCGCAG 637
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
190 eMetAspAspPheThrProSerGlyGlnThrAspIleValAlaLeuProG 207
638 GCGGACAGAGAGAACCAAGACAGACCTCCACCTATGTGACATACCTAT 687
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207 LysArgThrThrValAsnProGlnAspProSerTyrValAspValThrTyr 223
688 GACTTCATCATTCGTGGCAACCACTTCTTACACTATGCAACTCATCAT 737
|||||:|||||:|||||:|||||:|||||:|||||:|||||
224 AspPheIleIleLysArgLysProLeuPheTyrThrIleAsnIleIleI 240
738 CCCCTGCGTACTCATCACCTCGCTGGGCATCTGCTTCTTACCTGCCCT 787
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240 eProCysValLeuIleThrSerLeuAlaIleLeuValPheTyrLeuProS 257
788 CAGACTGTGTGAAGAAGTGAACACTTGTATTTCTGTCTGTCTAGTACTG 837
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257 eArgPheGlyGlnLysMetThrLeuCysIleSerValLeuLeuAlaLeu 273
838 AGCGTGTCTGCTGCTCATCTGCAAGATGTGCTCCACCTCCCTGGA 887
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888 TGAACCGCTGGTGGCAAGTACCTCATGTTTACATGCGTGAAGTACCT 937
|:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
290 rIleProLeuIleGlyLysTyrLeuLeuPheThrMetValIleValThr 307
938 TCTCATGCTGCACAGCGTGTGTCTCATATGTGCACACCGCTCGCT 987
|||||:|||||:|||||:|||||:|||||:|||||:|||||
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988 ACCAGCACACCATGAGCCCTGAGTCAAGTGTCTTCTTCCGAGAACT 1037
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1038 GCCACACCTGCTCTCTGTCAGACAGCCACGSCACCGCTGTCACGCTAGC 1087
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340 uProThrPheLeuPheMetLysArgProGlyLeuGlnValIleSerLeuVal 357
1088 GT.....CTGCGCTAGAGAGCGCCAGGAGAGAGCT 1119
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357 rGlyValProHisProSerGlnLeuHisLeu..... 366
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367 .....AlaPheAlaAspThrAlaAlaThr 374

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187	altrhphepPhepPheapspgInglInAnscysLysmellysPheclYser	203
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204	trpPhrtyrLyspLysAlaLysLLeaspLeuclLmeclLugIntrrVa	220
585	CAGCTGGATGATTCACACACCGAGGGAGATGGAGCATCAGCAGC	634
220	LaspLeuLysAspTryrTrpLglLuseLglLutrrAlaLLevalAsnAlat	237
635	CAGGGCCAGCAACAGAGAACCCAGACGAC.....TCACATATGTG	675
237	hrgLylrThrLysAsnSerLysLysTryrAspScyAlaGluLleLrrPro	253
676	GACATCAGCATATGACTTCATCTTCGTGGCAAAACAGACTCTCTACATAT	725
254	AspValrThrTrpAlaPheValLLeLrrArgLrLeuProLrLeuPheLrrThrl	270
726	CACCTCATCATCCCCGTGGTACTATACCTGCTGGCATCTGAGTCT	775
270	asnLueLlelLerProCysLeuLleLlLerCysLLeuTrhValrLLeuValr	287
776	TCACAGTCGCGCTAGACTGTGGTGAAGAAGATGACACTGTGTATTCCTG	825
287	heryLLeuProserAspScyLglLylLysLlLerThrLencysLlLerVal	303
826	CTGGCAGACATCAGAGGTCTCTGCTGTCATCTCCAGATGTGTGCTCC	875
304	LeuLueSerLrLeuThrValrPheLleuLleuLleuLlLerhGluLlelLerProse	320
876	CAGCTCCCTGATGTACCGCTGGTGGGAGATACCCATGATTTACCATAG	925
320	rThlSerLleuValLlLerProLleuLlLglLglLylLLeuLleuPheTrhMetl	337
926	TGCTAGTACACTTTCATCATCTGACACAGCGTGTGTGTGTCATATGGAC	975
337	LerPhValrThrlLLeuSerLlLLevalLlLerPhValrPheValrLLeuAsnValnls	353
976	CAGCGCTGGCTACACACACACACATAGGCCCCCTGGGTCAAGGTGCTT	1025
354	LlAspAspSerProserThrLlLlLrMetronlStrAlaLrrglLylAlale	370
1026	CTGGAGAAAGCTGCCACCTGCTCTTCTTCAGACAGCCAGC.....	1068
370	lLueLlLysLysLrrArgLrrLrrLleLlLlLerMetAsnAlaLrrProLrrPro	387
1069	.....CAGCGCTGGCAGCTGACAGCTGGC.....	1095
387	alGlLlLueCysLlLrrProLleuLrrLleuLysLLeuSerProserTrhTrlStrPr	403
1096	TrpAGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1145
404	LerLglLuseAsnValrLAspAlaLglLugLlLrrglLylValrLValrLglLugL	420
1146	AGGCTCGGCTGAGCAGCATGAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGT	1195
420	unsprrTrpTrpAla.....CysAlaLglLlLysValrAlaPro...SerValG	434
1196	AGGCTGGGCTGGGGGCTTCCAGAGTCAGAGCCAGCTGAGAGCGGGCGG...	1242
434	lYThrlLecCysSerhLlLglLlLlLlLlLlLlLlLlLlLlLlLlLlLlLlLlLl	450
1243	.....GGGGCTCTGTGGGGCCATGACAGCTGTGG	1271
451	AlaGlualLaleLueInglLugLlLglLylLLeuLLeu.....LeuSerTrhnl	465
1272	CTCTCGGAGAGACAGTGGATGGCGGTACCGCTTATTCGGGAGCCATCGGAA	1321
465	shetLl	482
1322	GTGAGCATGATGACACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1371
482	erGlLAspAlaAspSerSerValrLysLglLAspTrpLrrLysTrpValAlaLmeL	498

1372 GAGATACACGCGCGTTCGCGAGATCTTGTCTTTGCTGTTGG 1421  
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 499 VALLIENAPRIETHEUTRIEUPHEIHELLEVALYSHENUL 515  
 1422 GACCGTGGCATGTTCCTGACGCT 1446  
 |||||:|||||:|||||:|||||  
 515 YTHRIETLYEUPHEUTRIEUPRO 523

seq\_name: /SIDSI/gcgcdata/geneseq/geneseqp/AA1995.DAT: AAR73966

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seq_documentation_block:
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ID AAR73966 standard; protein; 529 aa.

AC AAR73966;

DT 30-NOV-1995 (first entry)

DE Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.

**KW** Human *nNACHr*; neuronal nicotinic acetylcholine receptor;

KW neurotransmitter.

OS Homo sapiens

PN W09513299-A.

PD 18-MAY-1995.

PF 08-NOV-1994: 94WO-US12859.

PR 08-NOV-1993; 93US-0149503.

PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.

PI Elliott KJ, Ellis SB, Harpold MM;

DR WPI; 1995-194036/25.

XX  
XX

used to develop prods. for detection, diagnosis and therapy and for

XX  
XX

XX  
PS Disclosure; Page 43-46; 34pp, English

CC human thalamus tissue

CC insert of one clone obcd. was ligated with the insert of another

CC used to identify hnACRs, cells contg. the DNA can be used for screening to identify cnds which modulate the activity of human

CC nNACHRS. The human nNACHR alpha 2 subunit can be used to produce antibodies which can be used in immunohistochemistry, diagnosis and

CC therapy. The nucleic acids can be used for analysing disease states and creating animal models

[illegible]

```
alignment_scores: 1000 00
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Ratio:	3.430	Gaps:	8
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US-07-938-154-10 x AAR

Align seq 1/1 to: AAR

85 ACTGACACAGAGGAGCGGCTAGTGAGCATCTCTTAGATCCCTCCCGCTA 134

56 ThrGluThrGluAspArgLeuPhelyshIleuPhe.....ArgGlyTy 70

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135  TAACAGCTGATTCCTGACCTGACTAAGCGCTGTGAGCTGTGACTGTAC 184
136  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
137  70  TAspAlaGlyProValArgProValArgProValArgProValArgProVal 87
138  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
139  185  AGCTCATGCTATCATTTGGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 234
140  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
141  87  rArgGlyLeuSerIleAlaGlnLeuIleAspValAspGlnLysAsnGln 103
142  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143  235  ATCATGACCAACATGCTGTGCTGACCCAGAGCTGGAGATTACCGCT 284
144  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
145  104  MetMetIleThrAsnValIleTrpLeuLysGlnIleTrpSerAspTyrLysLe 120
146  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
147  285  CACATGAGACCGCTGAGACTGTGACATATGAAAGTCCGCGCTCT 334
148  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
149  120  uArgTrpAsnProAlaAspArgLeuAsnIleThrSerLeuAlaGlyAlaPro 137
150  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
151  335  CCAACACATGCTGCTCCAGAGCTGTGCTATATGAAACATGCTAGCGC 384
152  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
153  137  ergIleMetIleThrIleProAspIleValLeuTyrAsnAsnAlaAspGly 153
154  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
155  385  ATGACCAAGCTCTCTCTATTCATGCTGTGCTGTGCTCTATGATGCGAG 434
156  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
157  154  GluPheAlaValIleThrIleMetThrLysAlaIleIleuPheSerThrGly 170
158  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
159  435  CATGCTTTGGCTACACCTGCTGCTACAGAGTGTGCTGCTGCTGCTGCTGCT 484
160  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
161  170  rValIleIleTrpValProProAlaIleTyrLysSerSerCysSerIleAsp 187
162  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
163  485  TGAAGCATTCCCATTTGACCAAGCAAGTTCACATGAAATTCGCTCA 534
164  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
165  187  alIleThrPheProPheAspGlnGlnAsnGlyLysMetLysPheGlySer 203
166  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
167  535  TGAAGCATTCCCATTTGACCAAGTTCACATGAAATTCGCTCA 584
168  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
169  204  TrpTrpIleAspLysAlaLysIleAspLeuLysGlnIleMetGlnIleTrp 220
170  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
171  585  CAGCTGTGATGACTTCACACCGAGGAGGAGTGGACATTCACGCTGCG 634
172  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
173  220  LAspLeuLysAspTyrTrpGlnSerGlyLysTrpAlaIleValAlaAsnAla 237
174  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
175  635  CAGCGCCAGCAGACGAGAACCCAGAC.....TCCACATATGTG 675
176  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
177  237  hrGlyIleTrpTyrAsnSerLysLysTyrAspCysAlaGlnIleTyrPro 253
178  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179  676  GACATCAGCTATGACTTCATCTATTCGTCGCAACCACTCTTCTACACTAT 725
180  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181  254  AspValIleThrTyrAlaPheValIleArgTyrLeuProLeuPheTyrThrI 270
182  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183  726  CAACCTCATCATCCCTGCTGCTCATCATCATCATCATCATCATCATCATCAT 775
184  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
185  270  eAsnLeuIleIleProCysLeuLeuIleSerCysLeuThrValLeuValP 287
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188  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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190  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
191  826  CTGCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 875
192  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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194  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
195  876  CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 925
196  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
197  320  rThrSerLeuValIleProLeuIleGlyLysIleLeuLeuPheThrMetI 337
198  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
199  926  TGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
200  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
201  337  IePheValIleThrLeuSerIleValIleThrValPheValIleLeuAsnAl 353
202  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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1026  CTGAGAGAGCTGCCCGCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1068
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1028  370  uLeuGlyCysValArgProAlaGlyTrpLeuLeuMetLeuAsnArgProProPro 387
1029  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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1031  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1032  387  aLgIleuLysAsnIleProLeuAlaGlyLeuLysLeuSerProSerTyrIleTrp 403
1033  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1034  1096  TTGAGAGAGCGCCAGCAGAGAGCTGAGCGCGAGCGGCTTTCTCTCTCTCT 1145
1035  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1036  404  LeuGlnSerAsnValAspAlaGlnIleArgIleValAlaValAlaGlnGlnI 420
1037  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1038  1146  AGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1195
1039  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1040  420  uAspArgTrpAla.....CysAlaGlyHisValAlaAlaPro...SerValG 434
1041  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1042  1196  AGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
1043  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1044  434  lYlThrLeuCysSerHisGlyHisIleHisLeuHisSerGlyAlaSerGlyPro 450
1045  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1046  1243  .....GGCGCTGTGAGCGCTGAGCCCACTGCGAGCGCTGTG 1271
1047  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1048  451  AlaGlnAlaLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1271
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1050  1272  CTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321
1051  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1052  455  sMeGlnLysAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 482
1053  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1054  1322  GTGAGAGATGATGACCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371
1055  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1056  482  ergIleAspAlaAspSerSerValLysGlnAspTrpLysTyrValAlaMet 498
1057  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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1060  499  ValIleAspArgIlePheLeuTrpLeuPheIleIleValCysPheLeuGln 515
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seq\_name: /STD1/gcgdata/geneseq/geneseq/AA1997.DAT:AAW09021

seq\_documentation\_block:

ID AAW09021 standard; Protein: 529 AA.

AC AAW09021:

DT 09-APR-1997 (first entry)

DE Neutonal nicotinic acetylcholine receptor alpha-2 subunit.

DE Neutonal nicotinic acetylcholine receptor; nAChR; neurotransmitter;

KW ligand-gated receptor.

KW

OS Homo sapiens.

PN WC9641876-A1.

PD 27-DEC-1996.

PE 07-JUN-1996; 96WO-0509775.

PR 07-JUN-1995; 95US-0484722.

PA (SIBI-) SIBIA NEUROSCIENCES INC.

PI Elliott KJ, Harpold NM;

DR WPI: 1997-065463/06.

DR N-PSDB; AAT18235.

PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units - used in screening to determine the effect of drugs on the receptor

XX Disclosure: Page 49-52; 108pp; English.

CC The alpha-2 subunit (AAW09021) of the human neuronal nicotinic  
CC acetylcholine receptor (nAChR) can be expressed in transformed  
CC host cells carrying alpha-2 subunit DNA (see also AAU48235). Host  
CC cells, esp. mammalian cells or amphibian oocytes, expressing the  
CC recombinant alpha-2 subunit, opt. in combination with other  
CC recombinant alpha and/or beta subunits (see also AAW09018-20,  
CC AAW09022-27) can be used to examine the function of human AChR and  
CC to identify cpts. that modulate its activity.

XX Sequence 529 AA:

alignment\_scores:  
Quality: 1221.00 Length: 475  
Ratio: 3.430 Gaps: 8  
Percent Similarity: 74.947 Percent Identity: 51.789

alignment\_block:  
US-07-938-154-10 x AAW09021 ..

Align seg 1/1 to: AAW09021 from: 1 to: 529

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70 rAnArgTrpAlaArgProValProAsnThrSerAspValValLeuValA 87
185 AGCGATGATATCATGTGGCTACAGCTATAGTGTGCACGAGCGGAGCGAG 234
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87 rGrPheGlyLeuSerIleAlaGlnLeuIleAspValAspGluLysAsnGln 103
235 ATGACACACCAATGTCTGTGGCTGAGCAGAGAGTGGGAAGATTACCGCT 284
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120 uAGTrpAsnProAlaAspPheGlyAsnIleThrSerLeuArgValProS 137
335 CCAAAACATCTGGCTCCAGATGTGGTCTATATCAACAATGCTGAGCGC 384
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137 eArgLysMetIleTrpIleProAspIleValLeuLysAsnAlaAspGly 153
385 ATGACGAAGTCTTCCTCTATTCGAATGCGTGGTCTCCATGATGGCAG 434
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154 GluPheAlaValIleThrIleMetThrLysAlaHisLeuPheSerThrGly 170
435 CATCTTTGGCTACACCTGCGCATCTACAAGAGTGCATGCAGATTGAGG 484
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170 rValHisTrpValProProAlaIleTyrLysSerSerCysSerIleAsp 187
485 TGAAGCACTCCCATTTGAGCAGACAGAAATGACCATGAAGTTGCTCTCA 534
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187 alThrPhePheProPheAspGlnGlnAsnCysLysMetLysPheGlySer 203
535 TGGACCTACGACCGTACTGAGATTGACCTGGTGTCAAAAAGTATGTGGC 584
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204 TrpThrTyrAspLysAlaLysIleAspLeuGlnMetGlnIleThrVal 220
585 CAGTCTGATGACTTACACCCAGCGGAGTGGAGCATCATCGACCTGC 634
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220 lAspLeuLysAspTyrTrpGluSerGlyLysTrpAlaIleValAlaSer 237
635 CAGGCCGACGCAAGAGAACCCAGACGAC.....TTCACCTATGTG 675
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237 hrGlyThrTyrAsnSerLysLysTyrAspCysAlaGluIleTyrPro 253

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676 GACATGACCTATGACTTCATCATTCGTGCAAAACCACTCTTACACTAT 725
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254 AspValThrTyrAlaPheValIleArgArgLeuProLeuPheThrTrp 270
726 CAACCTCATATCCCGGCTGACCTATGACCTGCGCCATCGCTGCTG 775
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270 eAsnLeuIleLeuProCysLeuLeuIleSerCysLeuThrValLeuVal 287
776 TCTACCTGCGCTGAGCTGTGGGAAAGATGACACTTGTATGTGG 825
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287 heTyrLeuProSerAspCysGlyGluLysIleThrLeuCysIleSerVal 303
826 CTGCTACACTCAGCGTGTCTGCTGCTCATCTCCAAAGATTGCTGCC 875
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 LeuLeuSerLeuThrValPheLeuLeuLeuIleThrGluIleLeuPro 320
876 CACCTCCCTGATGTACCGCTGCGGAGCAAGTACCTCATGTTCACATG 925
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
320 rThrSerLeuValIleProLeuIleGlyGlyLysTrpLeuPheThrMet 337
926 TGCTAGTCACCTTCTCCATGCTCACAGCGTGTGTGTCTCAATGTGCAC 975
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
337 LePheValThrLeuSerIleValIleThrValPheValLeuAsnValHis 353
976 CACGCTGCGCTTACCAGCAGACACATGCGCCCGTGGTCAAGTGGTCT 1025
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
354 HisArgSerProSerThrHisThrMetProHisTrpAlaArgGlyAla 370
1026 CTTGAGAGAGCTGCCACCGCTCTTCTGTCAGACACCGC..... 1068
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
370 uLeuGlyCysValProArgTrpLeuLeuMetAsnArgProProProPro 387
1069 ..CACCGCTGCGACGTCAGCGCTGCGC..... 1095
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
387 aGluLeuCysHisProLeuArgLeuLysLeuSerProSerTyrHisTrp 403
1096 TTGAGAGAGCGCCAGCAGAGACCTGAGGCGAGCGGCTTTCTTCGTGA 1145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
404 LeuGluSerAsnValAspAlaGluGluArgGlyValValGluGluGlu 120
1146 AGGTCTGCGGCTGACCCATGATGCTGCTTGTGCAACCTGCATCACTGC 1195
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
420 uAspArgTrpAla.....CysAlaGlyHisValAlaPro...SerValG 434
1196 AGGCGTGGCTGGGCTTTCGAGCTGAGCCGACCTGACCGCGCGCG... 1242
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
434 LysThrLeuCysSerHisGlyHisLeuHisSerGlyAlaSerGlyProLys 450
1243 .....GGCGGCTGTGGGCGCATGCACTGTGG 1271
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
451 AlaGluAlaLeuLeuGlnGluGlyGluLeu.....LeuSerProHis 465
1272 CCTCCGGGAGCAGCTGATGAGTGGCGCTTATGCGGACCACTGCGAA 1321
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
465 sMetIleLysAlaLeuGluGluGlyValHisTyrIleAlaAspHisLeuArg 482
1322 GTGAGGATGATGACAGAGTGTGAGGAGAGCTGGAATACGTTGCCATG 1371
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
482 eArgLysAspAlaAspSerSerValLysGluAspTrpLysTyrValAlaMet 498
1372 GTGATGCAACCGCTGCTGCTGTGATCTTGTCTGCTGCTGCTGG 1421
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
499 ValIleAspArgIlePheLeuTrpLeuPheIleIleValCysPheLeuG 515
1422 GACGCTGCGCATGTTCTGCTGCGCT 1446
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
515 YThrIleGlyLeuPheLeuProPro 523

```

seq\_name: /SIDS1/gcgdata/geneseq/geneseq/AA197.Dat:AAW1824

seq\_documentation\_block:

ID AAW1824 standard; Protein; 627 AA.  
XX

AC AAW1824:

XX 05-OCT-1997 (first entry)

XX Alpha4 subunit of normal nACHR.

XX nACHR: mutation; autosomal dominant nocturnal frontal lobe epilepsy;  
KM ADNFLE: neuronal acetylcholine receptor.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 280 /note= "Ser 248 Phe is the ADNFLE-  
FT inducing mutation (see AAW1825)"  
XX

XX AU9656247-A.

XX 09-JAN-1997.

XX 28-JUN-1996; 96AU-0056247.

XX 28-JUN-1995; 95AU-0003840.

XX (UYBO-) UNIV BONN.

XX (UYME-) UNIV MELBOURNE.

XX (ROME-) WOMEN'S &amp; CHILDREN'S HOSPITAL.

XX Berkovic SE, Mulley JC, Phillips HA, Propping PJ,  
XX Scheffer IE, Steinleinok, Sutherland GR, Wallace RM;  
XX WPI: 1997-100506/10.

XX N-PSDB: AAT59527.

XX CHRNA4 gene encodes neuronal nicotinic acetylcholine receptor  
PT fragment - used in diagnosis of autosomal dominant nocturnal frontal  
PT lobe epilepsy

XX Disclosure: Fig 13; 20pp; English.

XX The DNA sequence of the normal nACHR is given in AAT59527,  
XX the DNA sequence of the ADNFLE-inducing mutant is given in AAT59528.XX Mutations at codon 248, which have the effect of replacing  
XX serine by another amino acid (e.g. phenylalanine) in the sixth  
XX amino acid of the transmembrane domain 2 (M2) of the alpha4  
XX subunit of nACHR have been found to be associated with ADNFLE.  
XX The primers given in AAT59529 and AAT59530 were used in the  
XX amplification of part of exon 5.

XX Sequence 627 AA;

Alignment\_scores:

Quality: 1204.50 Length: 625  
Ratio: 3.238 Gaps: 14  
Percent Similarity: 59.520 Percent Identity: 42.720

Alignment\_block:

US-07-938-154-10 x AAW1824 ..

Align seg 1/1 to: AAW1824 from: 1 to: 627

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36 GGGCGCTTCACGCTTCCTTGGCTGCTGAGGGGTTTGGGA. 84
   ||||| :||| ||| ||| :||| ||| |||
7  GYAlAPrOArGLeuPrOleuLeuLeuLeuLeuGly.ThrGlyL 23
   .....ACTGACACAGAGAGCGG 102
85 .....
23 euleuAlaIaSerSerHsValGIuThrArGAlaHsAlaGIuArG 39
   .....
103 CTAAGTGGAGCATCTGTAGATCCCTCCGCTATAAGAGCTGATTCGCC 152
   ||||| :||| ||| ||||| |||||
40 LeuLeuLysLysLeuPhe.....SerGIyTrAsnLysTrpSerArGPr 54

```

```

153 AGCTACTAAGGGCTGTGAGCTGTGACTGTACAGCTCAATGATTCG 202
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
54 OValAlaAsnLIeSerAspValValLeuValArGpHeGlyLeuSerLIeA 71
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
203 CTCAGCTCATTTAGTGTGACAGCGGAGCAGATCATGACCAATGTC 252
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
71 LaGInLeuIleAspValAspGIuLysAsnGIuMetMetThrTrHsVal 87
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
253 TGGCTGACCCAGAGAGTGGAGATTAACCGCTCACATGAGAGCCTGAGA 302
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
88 TrpValGIuGIuGIuTrpHsAspTrpLysLeuArGTpAspProAlaAs 104
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
303 CTCGCAATGATGAGAAAGTCGGCTCCCTCCAAACACATCGGCTGCC 352
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
104 pLyGIuAsnValTrHsSerLIeArGIleProSerGIuLeuIleTrpArG 121
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
353 CAGATGTGTTCTATACAAACAAATGCTGACGGCATGTACGAAGTCTTC 402
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 roAspLIeValLeuTrpAsnAsnAlaAspGIyAspPheAlaValTrHs 137
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
403 TATTCCAATGCTGTGCTCCATGATGAGCAGACATCTTGGCTACGACG 452
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
138 LeuThrLysAlaHsIleuPheHsAspGIyArGIuGIuTrpHsProPr 154
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
453 TGGCATCTCAAGAGTGCATGCAGATGAGGTGAAGCACTTCCATTGG 502
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
154 oAlaIleTrpLysSerSerCysSerLIeAspValTrpPheProPheA 171
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
503 ACCAGCAGAAATGCACCATGATGTTGCTCATGAGCCTACAGCGTACT 552
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
171 spGIuInAsnCysThrMetLysPheGIySerTrpTrpThrTyAspLysAla 187
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
553 GAGATTGACCTGTG...CTCAAAAGTATGCGCCACTGTGATGATT 599
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
188 LysLIeAspLeuValAsnMetHsSerArGIyAlaSpGIuLeu...AspH 203
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 CACACCCAGCGGGAGTGGAGCATTCGACCTGCCAGCGGCAAGCA 649
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
203 eTrpGIuSerGIyGIuTrpValLIeValAspValaGIyTrpHsArG 220
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
650 AGAACCCAGACGAC.....TCCACCTAATGAGCATCAACCTATGAC 690
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 hArGIySyrTrpLysCysAlaGIuIleTrpProAspLIeThrTyAla 236
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
691 TTCATCATTCGTGCAAAACCACTCTTACACTATCAACTCATATCCC 740
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
237 PheValLIeArGIuArGIuProLeuPheTrpHsLIeAsnLIeLIePr 253
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
741 CTGCGTACTCATCATCTGCTGCGCATGCTGTCTTACCTGGCGCTAG 790
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
253 ocysLeuLeuLIeSerCysLeuThrValLeuValPheTrpLeuProSerG 270
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 ACTGTGGTGAAGATGACACTTGTATTTCTGTGCTGTGACACTACG 840
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
270 LucysLIuGIuLysLIeThrLeuCysLIeSerValLeuLeuSerLeuThr 286
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
841 GTGTCTCTGCTCATCTATCCAAAGATGTGCTCCACCTCCATGATCT 890
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
287 ValPheLeuLeuLIeHsGIuIleIleProSerThrSerLeuValLI 303
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 ACCGCTGGTGGGCAAGTCACTATGTATACATGAGTGTACTACCTTCT 940
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
303 eProLeuLIeGIyGIuTrpLeuPheTrpHsMetLIePheValTrHs 320
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
941 CCATGTCACAGCGTGTGTGTCATGTGACACCAACGCTGCCCTACCC 990
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
320 eTrLeuValLIeThrValPheValLeuAsnValHsHsArGIySerProArG 336
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
991 AGCAGACCATGAGCCCTGGTCAAGGTGCTTCCGGAAGAGCTGCC 1040
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337 TrHsHsThrMetProThrTrpValArGIuArGIuPheLeuAspLIeValPr 353

```







```

XX Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 280 /note= "Ser 248 Phe is the ADNFLE-
FT inducing mutation (see AAW11824)"
XX
XX A09656247-A.
XX
XX 09-JAN-1997.
XX
XX 28-JUN-1996; 96AU-0056247.
XX
XX 28-JUN-1995; 95AU-0003840.
XX
XX (UYBO-) UNIV BONN.
XX (UYME-) UNIV MELBOURNE.
XX (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
XX
XX Berkovic SF, Mulley JC, Phillips HA, Propping PJ;
XX Scheffer IE, Steinleinok, Sutherland GR, Wallace RH;
XX WPI: 1997-100506/10.
XX N-PSDB: AAT59528.
XX
XX CHRNA4 gene encodes neuronal nicotinic acetylcholine receptor
XX fragment - used in diagnosis of autosomal dominant nocturnal frontal
XX lobe epilepsy
XX
XX Disclosure; Fig 13; 20pp: English.
XX
XX The DNA sequence of the normal nACHR is given in AAT59527,
XX the DNA sequence of the ADNFLE-inducing mutant is given in AAT59528.
XX Mutations at codon 248, which have the effect of replacing
XX serine by another amino acid (e.g. phenylalanine) in the sixth
XX amino acid of the transmembrane domain 2 (M2) of the alpha4
XX subunit of nACHR have been found to be associated with the ADNFLE.
XX The primers given in AAT59529 and AAT59530 were used in the
XX amplification of part of exon 5.
XX
XX Sequence 627 AA:
XX
XX Alignment-scores:
XX Quality: 1198.50 Length: 625
XX Ratio: 3.230 Gaps: 14
XX Percent Similarity: 59.360 Percent Identity: 42.560
XX
XX alignment_block:
XX US-07-938-154-10 x AAW11825 ...
XX
XX Align seg 1/1 to: AAW11825 from: 1 to: 627
XX
XX 36 GCGCGTGTACGCTTCAGCCCTCTTTGGCGTGTCTTACAGGCGTTTGGGA. 84
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 7 GYAlaIaPrOvArgLeuLeuProPheLeuLeuLeuLeuLengly. ThrGlyL 23
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 85 .....ACTGACACAGAGGAGCGG 102
XX :::::|||||
XX 23 euleuAArgAlaSerSerHisValGluThrArgAlaHisAlaGluGluArg 39
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 103 CTATGAGGAGCATCTCTATGATCCCTCCCGGTATACAAACATGATTCGCC 152
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 40 LeuLeuLysLysLeuPhe.....SerGlyTyrAsnLysTyrSerArgPr 54
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 153 AACTTACTTAAAGCGTCTAGCGTGGTGGAGTACATGACGATGATGATGCG 202
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 54 ValAlaIaAsnIleSerAspValValIleValAlaIaIleGlyLeuSerIleA 71
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 203 CTGACGCTATAGTGTGACGAGCGGAGGAGCATGATGACACCAATGTC 252
XX |||||:::||||| ||| ||| ::||| ||| |||
XX 71 IAGlIleuIleAspValaIaSpIuIlysaSngIInmeIeThrThrIhrSnaI 87

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[illegible]

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387 GLuProGluGluGluProProAlaThrSerGlyThrGlnSerLeuHisSpr 403
1095 .....
403 oProSerProSerPheCysValProLeuAspValProAlaGluProGlyP 420
1095 .....
420 roSerCysSerProSerAspGlnLeuProGlnGlnProLeuGlu 436
1095 .....
437 AlaGluLysAlaSerProHisProSerProGlyProCysAspProPron 453
1096 .....
453 sGlyThrGlnAlaProGlyLeuAlaLysAlaArgSerLeuSerValGln 470
1109 AGCGAGAGCGGTGAGGCGGCGGCTTTCTCCGTGAGGT ..... 1149
470 lsmetSerSerProGlyGluAlaVal ..... GluGlyGlyValArg 483
1150 .....
484 CysArgSerArgSerTleGlnTyrCysValProAlaGlyAspAlaAlaPr 500
1152 TCAGCGGTGAC ..... 1161
500 oGluAlaAspGlyGlnAlaAlaGlyAlaLeuAlaSerArgAsnThrHis 517
1162 .....
517 eAlaGluLeuProProProAlaAspGlnProSerProCysLysCysThrCys 533
1174 TTGTGACCCCTGCATGCAGTGCAGGCTTGAGTGGGCGCTTCGAGGTGA 1223
534 LysLysGluProSerSerValSerProSerAla...ThrValLysThr 549
1224 GCCCACTGCAGCCGCGCGGCGCTGTGTGGCCATGCAGCTGTGGCC 1273
549 gSerThrLysAlaProProHisLeu.....ProLeuSerProAlaL 564
1274 TCAGGAGACAGTGAAGTGCATGCATGCATGCATGCATGCATGCATGCAT 1323
564 eutThrArgAlaValGlnGlyValGlnTyrIleAlaAspHisLeuLysAla 580
1324 GAGGATGATGACACAGATGATGAGAGAGTGAATATGATGATGATGATG 1373
581 GluAspThrAspPheSerValLysGlnAspTrpLysTyrValAlaMetVa 597
1374 GATCGACCCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATG 1423
597 lIleAspAlaGlnPheLeuTrpMetPheIleValCysLeuLeuGlyT 614
1424 CCGTCGCGATGTTCTCGACGCT 1446
614 hTValGlyLeuPheLeuProPro 621
seq_name: /SIBS1/gcgdata/geneseq/geneseq/AA1997.DAT:AAW09022
seq_documentation_block:
ID AAW09022 standard; Protein: 504 AA.
XX
AC AAW09022:
XX
DT 09-APR-1997 (first entry)
XX
DE Neuronal nicotinic acetylcholine receptor alpha-3 subunit.
XX
KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
XX ligand-gated receptor.
XX

```

```

OS Homo sapiens.
XX
PN W09641876-A1.
XX
PD 27-DEC-1996.
XX
PF 07-JUN-1996; 96MO-US09775.
XX
PR 07-JUN-1995; 95US-0484722.
XX
PA (SIBS1) SIBIA NEUROSCIENCES INC.
XX
PI Elliott KJ, Harpold MM;
XX
DR WPI; 1997-065463/06.
XX
DR N-PSDB; AAT48236.
XX
PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
XX used in screening to determine the effect of drugs on the receptor
XX
PS Disclosure; Page 54-56; 108pp; English.
XX
CC The alpha-3 subunit (AAW09022) of the human neuronal nicotinic
XX acetylcholine receptor (nAChR) can be expressed in transformed
XX host cells carrying alpha-3 subunit DNA (see also AAT48236). Host
XX cells, esp. mammalian cells or amphibian oocytes, expressing the
XX recombinant alpha-3 subunit, opt. in combination with other
XX CC AAW09023-27), can be used to examine the function of human AChR and
XX to identify cpds. that modulate its activity.
XX
SQ Sequence 504 AA:

alignment_scores:
Quality: 1179.50 Length: 495
Ratio: 3.223 Gaps: 7
Percent Similarity: 73.939 Percent Identity: 47.071

alignment_block:
US-07-938-154-10 x AAW09022 ..
Align seg 1/1 to: AAW09022 from: 1 to: 504

55 CTCTTTGGCTGCTCAGGCGTTTGGAGACTGACAGAGAGCGGCT 104
||||| ||| .....:|||||
21 LeuSerLeuLeuProValAlaArgAlaSerGluAlaGlnHisArgLe 37
105 AGTGAGAGTCTTAGATCCCTCCGCTATACAGCTGATTCGTCAG 154
| |||:|||||:
37 upheGluArgLeuPheGluAsp....TyrAsnGluIleIleArgProV 52
155 CTACTAACGCTCTGAGCTGTGAGCTGTACAGCTCATGATATGCT 204
:||||| |||: .....:
52 AlaAlaAsnValSerAspProValIleIleHisPheGluValSerMetSer 68
205 CAGCTATTAGTGTGACAGAGCGGAGACAGATCATGACACCAATGTG 254
|||||:||||| ||| .....:|||||
69 GlnLeuValLysValAspGluValAsnGlnIleMetClnThrAsnLeuTr 85
255 GCTGACCCAGAGTGGAGATTACCGCTTCACATGAGAGCTGAGAGT 304
||||| ||| |||:|||||:||||| |||:|||||:
85 PheLysGlnIleTrpAsnAspTyrLysLeuLysTrpAsnProSerAspT 102
305 TCGACAAATATGAGAAAGTCGCGCTCCCTTCAACACATCTGCTCCA 354
::: |||: |||: |||: |||: |||: |||
102 YrGlyGlyAlaGluPheMetArgValProAlaGlnLysIleTrpLysPro 118
355 GATGTGCTTATACAAATGCTGAGCGATGATGAGAGCTCCCTTGA 404
|||||:||||| ||| .....:|||||
119 AspIleValLeuTyrAsnAlaValGlyAspPheGlnValAspAspLys 135
405 TTCCAATGCTGTGCTCTATATGATGACAGATCTTTGGCTACCACTG 454

```



CC human neuronal nicotinic acetylcholine receptor (nAChR) was deduced  
 CC from a DNA clone (AA048232) isolated from a human substantia nigra  
 CC cDNA library. A variant (del174-88) alpha-6 subunit (AA09019) was  
 CC also identified. Recombinant alpha-6 subunits can be expressed in  
 CC host cells, esp. mammalian cells or amphibian oocytes, optionally  
 CC with beta-3, beta-1 and/or beta-2 subunits (see also AA09020,  
 CC AA09026-27). The recombinant subunits and host cells can be used to  
 CC study the function of the human nAChR and to identify cpos. Chat  
 CC module its activity.

XX Sequence 494 AA:

alignment\_scores: Quality: 1163.00 Length: 495  
 Ratio: 3.195 Gaps: 9  
 Percent Similarity: 73.535 Percent Identity: 47.071

alignment\_block:  
 US-07-938-154-10 x AA09018

Align seg 1/1 to: AA09018 from: 1 to: 494

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58 CTTGGCTGTC.....TCAGGGTTTGGGAACGTA 89
16 LeuTrpLeuCyValPheThrProPheHesGlyValGlyCysAl 32
90 CACAGAGAGCGGAGTATGAGCATCTTATGATCCCTCCGCTATAGA 139
32 aTrpGluGluAlaTrpLeuPheHisIleTrpAsnAspTrpGlyLeuAla 47
140 AGCTGATGTCGACGCTATACGAGCTGTGAGTGTGATGATGACGCTC 189
47 IahPheIleAlaProValGluAsnValSerAspProValIleValHisPhe 63
190 AUGGTATCATGGCTCAGCTCATTTAGTGTGACAGCGGAGGAGATGAT 239
64 GluValHisIleThrGlnLeuAlaAsnValAspIleValAsnGlnIlePhe 80
240 GACCAACCAATGTCGTGAGCCAGAGAGTGGAGATTCAGGCTCAGAT 289
80 GgIuTrpAsnLeuTrpLeuAlaGlnHisIleTrpAsnAspTrpGlyLeuAla 97
290 GGAAGCTGAGGAGCTGACAAATATGAAGAAGTCCGGCTCCCTGCAAA 339
97 TrpAspProMetGluTrpAspGlyIleGluTrpLeuAlaGlyAlaProAlaAsp 113
340 CACATGTCGCTCCAGATGTCGTCATATACAAATGTCGACGCAATGA 389
114 LysIleTrpLeuProAspIleValIleuTrpAsnAlaValGlyAspHis 130
390 CGAAGTCCTCTATTCGAATGCTGGTGGCTGCTATGATGAGGAGATG 439
130 GgIuValGluGlyLysTrpLysAlaLeuLeuLysTrpAsnGlyMetIleTr 147
440 TTGGCTACCACTCCATCTACAAAGATGATGCAAGATGAGTGAAG 489
147 hTrpTrpProAlaIlePheLysSerSerCysProMetAspIleThr 163
490 CACTTCCATTTGACCCAGAGATTTGACATGAGTTCGTCATGAGAC 539
164 PhePheTrpPheAspHisGlnAsnGlySerLeuPheGlySerTrpHis 180
540 CTACGACGCTAGTATGATGATGATGATGATGATGATGATGATGATG 589
180 TrpTrpAspLysAlaGluIleAspLeuLeuIleIleGlySerLysValAspHis 197
590 TGATGATCTCACACCCAGCGGAGTGGGACATGATGACGCTGAGGAC 639
197 GtAsnAspPheTrpLysSerGlyTrpGluIleIleAspAlaSerGly 213
640 CGACGCAACGAG.....AACCCAGACGACTCCACATGATGAGCAT 680

```

```

214 TrpLysHisAspIleLysTrpAsnGlyGluIleIleTrpHisAspI 230
681 CACCATGACATTCATCATATGCTGCCAAACCACTCTTCTACATATCAAC 730
230 TrpTrpSerPheTrpLysAlaGlyLeuProMetPheTrpHisAla 247
731 TCATATCCCTCCGCTACTCATCTGCTGGCCATCTGATGCTTTCAC 780
247 GtIleIleProCysLeuPheIleSerPheLeuThrValLeuValPheTrp 263
781 CTGCGCTCAGACTGTGTGAAGAATACACTTTGATTTCTGTCTGCTCT 830
264 LeuProSerAspCysGlyGlyValThrLeuCysIleSerValLeuLe 280
831 AACACTCAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
280 uSerLeuThrValPheLeuLeuValIleThrGluThrIleProSerHis 297
881 CCGTCGATGTACCGCTGTGGGAGCAAGTCAATGTTTACATGCTGCTA 930
297 GtLeuValValProLeuValGlyIuTrpLeuLeuPheThrMetIlePhe 313
931 GTACCTTCTCCATGCTGACCAACGCTGTGTCTCATATGTCACACCG 980
314 ValThrLeuSerIleValAlaThrValPheValLeuAsnIleHisTrpAl 330
981 CTGCGCTACCAAGCAACATGAGCCGCTGCTGCTGCTGCTGCTGCTG 1030
330 gThrProThrThrHisTrpMetProAlaGlyValLysThrValPheuL 347
1031 AGACATGCGCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1077
347 yLeuLeuProGlnValLeuLeuMetAlaGTrpLeuAsnTrpLysHis 363
1078 .....GCAAGTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
364 GluThrGlySerAspAlaValProAlaGlyLeuAlaAlaGlyAla 380
1113 AGAGCT.....GAGGAGAGCGGCTTTCTTCGTAAGTCTCTG 1153
380 GgIuLysLeuAlaSerHisGlyLysProAlaGlnHisLeuLysGlu 394
1154 CGGTCGACCATGTCACCTGCTTGTCAACGCTGATCATGTCAGGAGCT 1203
395 .....CysPheHisCysHisLysSerAsnGlu...Leu 404
1204 GCTGGGCTTCCGA.....GCTGA 1223
405 AlaThrSerLysAlaGlyLeuSerHisGlnProLeuGlnTrpValVal 421
1224 GCGCACTGACCGCGCGCGCGGCTGTGGGCGCATGACAGTGTGGC 1273
421 uAsnSerGluHisSerPro.....GluV 429
1274 TCCGGGAAGCAGTGAATGCGTACGCTTACATTCGCGACCATGGAAGT 1333
429 aGlnAspValIleAsnSerValGlnPheIleAlaLysMetLysSer 445
1324 GAGGATGATGACAGAGTGTAGGAGAGAGATGGAATATAGTTCGATG 1373
446 HisAsnGluThrLysGluValGluAspAspTrpLysTrpValAlaMetVal 462
1374 GATGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1423
462 lValAspTrpValPheLeuTrpValPheIleIleValCysValPheGly 479
1424 CCGTGGCATGTTCTGACGCTCTCTCCAGAAC 1458
479 hAlaGlyLeuPheLeuGlnProLeuLeuGlyAsn 490

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seq\_name: /SIPSI/gcgdata/geneseq/geneseq/AA1994.DAT:AAW44152  
 seq\_documentation\_block:











GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 03:06:12 ; Search time 127.69 Seconds

(without alignments)  
7435.095 Million cell updates/sec

Title: us-07-938-154-10

Perfect score: 1512

Sequence: 1 ATGCTGGCTTGCATGCGCGG.....CAGCTCCAGCTCCTCAAGTGA 1512

Scoring table: IDENTITY\_NDC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : N\_Geneseq\_0601.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1162.6	76.9	1521	AA014288	Human neuronal nlc
2	1159	76.7	2448	AAV12201	Human neuronal nlc
3	1159	76.7	2448	AAV18240	Human neuronal nlc
4	691.8	45.8	1915	AAV12198	Human neuronal nlc
5	691.8	45.8	1915	AAV18241	Human neuronal nlc
6	648.6	42.9	2460	AA006086	Plasmod p2PC13 enc
7	452.6	29.9	2277	AAV12199	Human neuronal nlc
8	452.6	29.9	2277	AA090387	Alpha 2 subunit of
9	452.6	29.9	2664	AAV18235	Neuronal nicotinic
10	434.2	28.7	2082	AAV18237	Alpha4 subunit of
11	434.2	28.7	3496	AAV18237	Neuronal nicotinic

12	432.6	28.6	2082	18	AAV18238	Alpha4 subunit of
13	419.8	27.8	2363	15	AAV12196	Human neuronal nlc
14	366.8	24.3	1908	18	AAV18236	Neuronal nicotinic
15	350.8	23.2	1757	15	AAV12200	Human neuronal nlc
16	342.2	22.6	1743	18	AAV18232	Neuronal nicotinic
17	338.8	22.4	3649	6	AAV18232	Neuronal nicotinic
18	331.6	21.9	1746	11	AAV18232	Neuronal nicotinic
19	331.6	21.9	1667	21	AAV18232	Neuronal nicotinic
20	301.2	19.9	1698	18	AAV18233	Neuronal nicotinic
21	281.6	18.6	3109	21	AAV18233	Neuronal nicotinic
22	266.4	17.6	1925	18	AAV18234	Neuronal nicotinic
23	256.4	16.9	1350	17	AAV18284	Neuronal nicotinic
24	254.8	16.9	1350	14	AAV18284	Neuronal nicotinic
25	254.8	16.8	1350	14	AAV18284	Neuronal nicotinic
26	242	16.0	3700	21	AAV18284	Neuronal nicotinic
27	234.6	15.5	1839	21	AAV18284	Neuronal nicotinic
28	230.8	15.3	1350	15	AAV18284	Neuronal nicotinic
29	228.6	15.1	1938	17	AAV18284	Neuronal nicotinic
30	220.6	14.6	1828	18	AAV18284	Neuronal nicotinic
31	212.6	14.1	2101	18	AAV18284	Neuronal nicotinic
32	211	14.0	1509	22	AAV18284	Neuronal nicotinic
33	210	13.9	1876	15	AAV18284	Neuronal nicotinic
34	209.4	13.8	1509	22	AAV18284	Neuronal nicotinic
35	209.4	13.8	1509	22	AAV18284	Neuronal nicotinic
36	209.4	13.8	1509	22	AAV18284	Neuronal nicotinic
37	209.4	13.8	1876	18	AAV18284	Neuronal nicotinic
38	207.8	13.7	1509	22	AAV18284	Neuronal nicotinic
39	206.2	13.6	1590	22	AAV18284	Neuronal nicotinic
40	203.4	13.5	2886	21	AAV18284	Neuronal nicotinic
41	203	13.4	2769	15	AAV18284	Neuronal nicotinic
42	155.8	10.3	1416	22	AAV18284	Neuronal nicotinic
43	137.4	9.3	705	19	AAV18284	Neuronal nicotinic
44	137.4	9.1	690	19	AAV18284	Neuronal nicotinic
45	108.6	7.2	1464	22	AAV18284	Neuronal nicotinic

#### ALIGNMENTS

RESULT 1	AA014288	standard; DNA; 1521 BP.
ID	AA014288	
XX	AA014288	
AC	AA014288	
XX	16-JAN-1992 (first entry)	
DE	Human neuronal nicotinic acetylcholine receptor beta 2 subunit.	
XX		
KW	hnnachr; ss.	
XX		
PN	WO9115602-A.	
XX		
PD	17-OCT-1991.	
XX		
PF	03-APR-1991; 91WO-US02311.	
XX		
PR	03-APR-1990; 90US-0504455.	
XX		
PA	(SALK ) SALK INST BIOTECHN.	
PI	Harpold MM, Ellis SB, Brust P, Akong M, Velicelebi G;	
XX	WPI; 1991-325241/44.	
XX		
PT	Human neuronal nicotinic acetylcholine receptor sub-units and	
XX	DNA - used for screening for agonists or antagonists for the	
PT	receptors.	
XX		
PS	Claim 5; Fig 9; 61pp: English.	
XX		
CC	The DNA sequence encodes the beta 2 subunit of the human neuronal	
XX	nicotinic acetylcholine receptor (hnnachr). The sequence was	



FR 08-MAR-1993: 9305-0028031.  
XX  
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
PA (SIBT-) SIBIA NEUROSCIENCES INC.  
XX  
XX Elliott KJ, Ellis SB, Harpold MM;  
PL  
DR WPI: 1994-303024/37.  
XX  
XX P-PSDB; AAMA44157.  
DR  
XX  
PT Human neuronal nicotinic acetylcholine receptor subunits and DNA -  
PT also transformed cells useful for screening cpds. which modulate  
PT activity of the receptor  
XX  
XX  
XX  
XX Example 2; Page 82-83; 99pp; English.  
XX  
XX The present sequence encodes a human neuronal nicotinic acetylcholine  
XX receptor (NACnR) subunit. The cells expressing the alpha and/or beta  
XX NACnR subunits may be used in a method of screening compounds to  
XX identify any which modulate the activity of human neuronal NACnR.  
XX Subunit specific antibodies may be used to monitor the distribution  
XX and expression density of various subunits in normal vs diseased brain  
XX tissues. Testing of single receptor subunits or specific receptor  
XX subunit combinations with a variety of potential agonists or antagonists  
XX provides information with respect to the function and activity of the  
XX individual subunits and should lead to the identification and design  
XX compounds that are capable of very specific interaction with one or  
XX more receptor subtypes. The resulting drugs should exhibit fewer  
XX unwanted side effects than drugs identified e.g. screening with cells  
XX that express a variety of subtypes.  
XX  
XX Sequence 2448 BP; 457 A; 801 C; 705 G; 485 T; 0 other;

	Query Match	Similarity	76.7%:	Score 1159:	DB 15	Length 2448:
	Best Local	Similarity	85.8%:	Pred No. 4,2e+294:		
	Matches 1312:	Conservative	0:	Mismatches 190:	Indels 9:	Gaps 3
OY	11	GCATGGCGGSGACACTCCAACTCAATGGCGCTGTTC--AGCTTACGCCCTTTTGCGTGT	67			
Db	263	gcattggcggcgagcgtgcccgccttgctcccttggcttcggcgtccctccgcgctg	322			
OY	68	GCTCAGGGGTTTTGGGAACAGACACAGAGAGCGGCTAGTAGAGCAATCTTAAATCCCT	127			
Db	323	gtctaaagggtgtgggtttacgatacacaggaagcggtctgtgtgaacatctcttgtatcctt	382			
OY	128	CCCCCTTAACAAGCTGATATTGTCGACGATACACAGGCGCTGAGCTGTGACTGTACAGC	187			
Db	383	cgcgtcaacaagaacttatctccgccagccaccaatlygctctlgagtctgtgaaccatlaagc	442			
OY	188	TGATGATATATTGGCGCACACTCATTAAGTGTGCACAGACGGGAGACAGTCTACGCCACA	247			
Db	443	ttagtgytacctgccccagctcatcagtgatgycatgagcgaggagatcalgaccaca	502			
OY	248	ATGTCGTGGCTGACCCACAGAGAGTGGGAAGATTACCGGCTGCACATGGGAAGCGTAGACATTGC	307			
Db	503	atgctgtgcctgcaccocaggaigtgggaagatlatctgccttaaccttgaagctgaagaagtltg	562			
OY	308	ACATATGAAGAAGATCCCGGCTGCCCTTCCAACAACATATGGCTGCCAGATGGTGTCTAT	367			
Db	563	aacaaatgaagaagaatctgcgtccctccccaacaacatctgcgtcccaatgctggtccctgt	622			
OY	368	ACAAATGCTGACGCGCATSTACGAAGTCTCTTATTCCAATBCTGTGTTCTCTATG	427			
Db	623	acaaaatgctggaaggaatgtaaagatgctctctcatctcaaatgacgttgctccctatg	682			
OY	428	ATGGCAGCAATCTTTGGCTACGACGTCGCCATTCACANAAGTAGTCATGACAAGATTGAGGTGA	487			
Db	683	atggcagcaatctctctgtcgtcgctgcacatctacaagaagcgaatgcaagattgaataa	742			
OY	488	AGCACTTCCATTGGACACAGATAAATTGGACCATTAAGTTTTCGCTTCANAGACTACACACC	547			

Db	743	agcaattccattctgacccaagaacgacgcacacatgaattccgtttctgtagccataagacc	802
Qy	548	GTACTGAGATTGACCGGAGGCTCAAAAGTATATGTGGCAGTGTGGATATATTTTACACCCA	607
Db	803	gacacagatgcacttgcttgtagaaggttagaggttgccagcccttgagacttaacaccta	862
Qy	608	GCGGGAGTGGACATCATATGCGACTGCGCAGGCGGACGCAACGAAACCCAGACATTTCCA	667
Db	863	gtggttgagtggaagacacgtagcgctgcgcgggcgcgcgcacaaagagaaaccccgacactcta	922
Qy	668	CTTATGTGGACATCACATTTGACTTTTCAATGTTGTGGCAACCAACTCTTTTACACTATCA	727
Db	923	ctgaagtgagacataacgatacttaacttaacttcgcgcgaagacgcgtctcttaacaccta	962
Qy	728	ACCTCATTCATCCCTCGCTACTCATACCTCGCTGGCCATCTCGTGTCTTCTACCTGCCCT	787
Db	983	acctcatcatcccttgtagcttaacacctgcgtatacctcttctcttaacttcgcat	104
Qy	788	CAGACGTGGTGAAGAAAGATATGACATTTGTATTTCTGTGCTGTGTACACTCATCGGTATTC	847
Db	1043	ccagacttgtagaagaagatagactgttgcatctcaagttgctgtgtagcgtctcc	110
Qy	848	TGCGTCATATCTCAAGATATTTGGCTCCCACTCCCTCATATACCGGTGTGGGCAAGT	907
Db	1203	tgctgtcatcttccaaagatcgtgtcctccacccctctcgagctgtgcgtctgtagaagt	116
Qy	908	ACCGCATGTTTACATATGGGTGATGACACTTTTCATGCTGACACAGGTGTGTGTGTCA	967
Db	1163	acctcatgcttaacatagttgcttgttaaccttccatctgtaacacaggtgtgtagtctca	122
Qy	968	ATTTGACACCAACGGCTCGCTACACGCACACATATGGCCCCCTTGGGTCAAGGTGATTC	102
Db	1223	acgtgacacacgcgtcgcgcgaacgaagacacaaaggcgtgggttgaaagtcgcttcc	128
Qy	1028	TGGAGAGTGTGCCACACTGCTGCTTTCTGTGACAGCACGCCACGCCCTGTGTACAGTACG	108
Db	1283	ctgagaaagcttcgcgcgcgtccttaacgtgaagacacgcacatcatgtgcgcgcgttaagc	134
Qy	1088	GTCGTGCTTTGAAGAGGCGCCAGCGAGAGCGTAGAGGC---GAGCGGATTTTCTTCCTGG	114
Db	1343	gctctgcctctgcgcgcgaacgcgaagcgtgaagcgaagagcgcgtgaagcctctctccgcg	140
Qy	1145	AAGGTCTCGGCGCTGACCCATGTAACCTGTAACCTGTTCACACCTTCATCACTAGTGAGGGCTTGG	120
Db	1403	aagcccccaaggcgccagctctccgaacgtagctctgtaacacgcgcgtctcgggtgaaggtttg	146
Qy	1205	CTTGGGAGTTTCCAGATGAGCCACTGGA---GCCGAGCCCGGGGGGCTCTGTGGGGCAT	126
Db	1463	ccggggccttcggggtcgtgaagccttgaccaagtgtagggccccgggcgcgtctcaaggagagcgt	152
Qy	1262	GCACTTGTGGCCCTCCCGGGAAGCAGTGGATGGCGTACAGCTTCATTTGCGAGCAACATTTGGAA	132
Db	1523	gttgctgtggtcctccggggggggtgtagcgcgtgtgcgtcttaacgcagaacacatgcyga	158
Qy	1322	GTGAGATGATGATGACAGATGTGAGGGAGACATCTGGAATAATATTTGTCATGATGGATGCACCC	138
Db	1583	ggcagagacgaatgacaaagacgttagtgtagaacctggaagtaagttgcgtatgtgtagcacc	164
Qy	1382	GCCCTGTTCCTGTGAGATCTTTGCTTTGTCTGTCTGTCTTGTGGAGCCGTCGAGATTTCTCG	144
Db	1643	gacctctccctcgtgatactttgtcttgctgtagtcttgtagcactatgggcaatggttctgtc	170
Qy	1442	AGCCTCTTCTCCAGAACTACATGCGACATCTTCTCTCCACCTTGACCACTACGTACGCTCCA	150
Db	1703	agctctctctccgaactatacaccaacacacttctctccactaagacacatcaagccccca	176
Qy	1502	GCTCCGAATGA 1512	
Db	1763	gtctcaaatga 1773	

RESULT  
AAT48240





Db	1111	ctacctctctctctcaatgaagccctgagcccgacagcagcccgccagagctctccgc	1170
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Db	1171	ccagacagtcatacgctgagccaaagcccgagccagccacactctccacagccctccaaact	1230
Qy	1154	cgccctacccactatgtaactcgtctttgtcaacctgcatactcagcagcgttgctt-----g	1207
Db	1231	tctatggaagaccbaatgtaactctgtgaaccccgctctgcagcttccaaactccagccgcg	1290
Qy	1208	ggcgctttccgagctcagccaccactgcacccgcccggcgccgctctgtagggccatgcagct	1267
Db	1291	gctctaccgccgttgycatctcccaagagattctctgctgcgtctctctggaagttccgac	1350
Qy	1268	gtgcgcttcggagagcagatgatggagggctgacgttatgtaggcagacacatnccgaatgag	1327
Db	1351	aggaatgtagagagagcatctgaagagcgctcagcttaccgcgcagccacaaatgaatgaag	1410
Qy	1328	atgatgaccacagactctgagagagactgcaaatatgactttccatgtagtgaacacgcctgt	1387
Db	1411	atgaagaccagagatctcgtctgagacttgaagaaatacgtgcatatgtgtgagccgctgt	1470
Qy	1388	tctctgcatcttcttctcttctgctctgctgtcttggagaccgttgagcatatttccagacc	1447
Db	1471	tctctgtaggtgtctatgtttgtgtgtgctctcgtgacactgtgtggctcttcttcgcgcgccc	1530
Qy	1448	tcttccagacatcactacgtccacacttcttccctccacccctgaccca	1490
Db	1531	tctctccagaccacatgacactctctgagggagcccttaacgtgcacca	1573

	RESULT	5
AAAT48241	ID	AAAT48241 standard; DNA; 1915 BP.
AC	AAAT48241;	
AD	09-APR-1997	(first entry)
AE	Neuronal nicotinic acetylcholine receptor beta-4 subunit DNA.	
AF	Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter,	
AG	ligand-gated receptor; ds.	
AH	Homo sapiens.	
AI	Key	Location/Qualifiers
AJ	CDS	87..1583
AK		/*tag= a
AL	WO9641876-A1.	
AM	27-DEC-1996.	
AN	07-JUN-1996;	96WO-US09775.
AO	07-JUN-1995;	95US-0484722.
AP	(SIBI-) SIBIA NEUROSCIENCES INC.	
AQ	Elliott KJ, Harpold MW;	
AR	WPI: 1997-065463/06.	
AS	P-PDB: AAM09027.	
AT	Nucleic acids encoding nicotinic acetylcholine receptor sub-units -	
AV	used in screening to determine the effect of drugs on the receptor	
AW	Disclosure: Page 83-85; 108pp; English.	
AX	A DNA sequence (AAAT48241) codes for the beta-4 subunit (AAM09027) c	
AY	the human neuronal nicotinic acetylcholine receptor (nAChR). Host	
AZ	cells, esp. mammalian cells or amphibian oocytes, carrying beta-4	

CC nucleic acids, opt. in combination with other alpha and/or beta  
CC subunit nucleic acids (see also AAT8232-40), express recombinant  
CC mChrr subunits useful for identifying cpds. that modulate the  
CC activity of human mChrrs.  
XX  
SQ Sequence 1915 BP; 374 A; 631 C; 505 G; 405 T; 0 other;

Query Match	45.8%;	Score 691.8;	DB 18;	Length 1915;
Best Local Similarity	67.7%;	Pred. No. 1.1e-171;		
Matches 1004;	Conservative	0;	Mismatches 467;	Indels 12;
				Gaps 2

[illegible]



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Db      1051  gctgcgccagacccacacacacacacacacacacacacacacacacacacacacacac 1110
Oy      1040  ccacccctgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1093
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Oy      1094  gcttgagagagccgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 1153
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Oy      1154  cgggtgacccacacacacacacacacacacacacacacacacacacacacacacacac 1207
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Db      1411  atgaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1470
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Db      1471  tccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1530
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Db      1531  tctccagacccatgacagctctctgtgagggccctacagctgcca 1573

RESULT 6
AA006086
ID      AA006086 standard; cDNA; 2460 bp.
XX      AC      AA006086;
XX      DT      24-JAN-1991 (first entry)
XX      DE      Plasmid p2PC13 encoding neuronal nicotinic acetylcholine receptor
XX      DE      beta 4 subunit.
XX      KW      Rat; nAChR; ss.
XX      OS      Rattus rattus.
XX      FH      Key      Location/Qualifiers
XX      FT      CDS      61..1548
XX      FT      sig_peptide 61..120 /*tag= a
XX      FT      mat_peptide 121..1545 /*tag= b
XX      FT      misc_feature 416..417 /*tag= c
XX      FT      misc_feature 1409..1410 /*tag= d
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FT      FT      /note="conflict between genomic and cDNA sequences"

W09010648-A.
20-SEP-1990.
14-MAR-1990; 90MO-US01403.
12-MAR-1990; 90US-0492555.
14-MAR-1989; 89US-0321384.
(SALK ) SALK INST FOR BIOL STUD.
Heinemann SF, Deneris ES, Duvoisin RM, Patrick JW;
WPI; 1990-304987/40.
P-PSDB; AAR07143.
New neuronal nicotinic acetylcholine receptor - compans. contg.
beta 4 sub-unit and DNA sequences encoding them.
Claim 11; Fig 3; 47pp; English.
The sequence encodes a novel neuronal nicotinic acetylcholine
receptor subunit, beta 4. Plasmid p2PC13 (ATCC 67893) was
isolated from a cDNA library in lambda ZAP II prep. from rat
mRNA. The sequence of the cDNA in the region encoded by the 5th
exon is identical to that determined for the genomic clone with
the exception of a sustn. at posn. 720 of a t for a c (this does
not alter the aa sequence); this may be due to a polymorphism
between the rat strains used for the genomic library and the cDNA
library, or could have resulted from a reverse transcriptase error
during prepn. of the cDNA. A sequence, the core of which is 44 bp
long is repeated three times at the beginning of the 3' UTR region.
The function of this remains unknown. The protein subunit can
combine with the known subunits, alpha-2, -3, and -4, and beta-2
to form previously unknown functional receptors. The new subunit
is expressed in the central and peripheral nervous systems and in
PC12 cells.
Sequence 2460 bp; 519 A; 767 C; 587 G; 587 T; 0 other;
Query Match 42.9%; Score 648.6; DB 11; Length 2460;
Best Local Similarity 66.5%; Pred. No. 2,7e-160;
Matches 958; Conservative 0; Mismatches 459; Indels 24; Gaps 1;
Oy      89  ACACAGAGAGAGCGCTAGTGGAGCATCTTAGATCCCTCCGGTATATACAGCGATTC 148
Db      131  acgcaagagaaagctgatagtatgatactcttgaaacaaacccggtacacacacatgacc 190
Oy      149  gtccagctactaacgctctgagctgctgctgctgctgctgctgctgctgctgctgctg 208
Db      191  gcccaagacacagctctctcctcctcctcctcctcctcctcctcctcctcctcctcctc 250
Oy      209  tcattagtgctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 268
Db      251  tcatcagtgtgatagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 310
Oy      269  gggaagattaccgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 328
Db      311  ggaactgactacgcctgctggaacagcctcctcctcctcctcctcctcctcctcctcct 370
Oy      329  tcccttccaaacacatctgctccacagatgtgcttattacacacatgctgacgacatgt 388

```

D	371	tcctccgcaaaagcg	tgtctgtgtctgtccatcgtgtgttlaaacaatgcccgaatctgcaact	430
D	389	ACGAAATCTCCCTTCTATTCCTCAATGCTGTGGTCTCCATGATGAGGAGCATCTTTTGGCTAC		448
D	431	atgaagctgtctctcaacaacgctgattgtgcttcaacagcagatccaaigtgctgc		490
D	449	CACCTTCCTCTCAAAAGATCATGACAAGATTGAGGTGAACACTTCCATTGTGACACAC		508
D	491	cccctctatcaaaaggtgcctgcgaagatttgaggtgaagacttcccttccttcgacagc		550
D	509	AGAAATTGCACATGAAATTTTGGCTCATGAGCCACGACCGGATGATGATTTGATTTGACTGGTGC		568
D	551	agaagtcgaacctcaaatctgcctcttcctgcgaacctatgacaaacagggatttgatctgttc		610
D	569	TCAAAAGTATGTGGCCGCTGTGATGACTTACACACGAGGGGAGTGGGACATCATATGC		628
D	611	ttaaagcgcgccacgycacatcaatgaaattcaaccccagcggagaaavggaaactatgctg		670
D	629	CATTCGCAGCCGAGCAGCAGCAAGAACCCAGACGATCTCAACTATGTGGACATCATATGAC		688
D	671	cccctccaaaggagggagcgggtgaaaccttgaagaccacgaagctacagctgaaatgaaactaag		730
D	689	ACTTTCATCTTGTGTCGCAACCACTCTTTTACACTATCAACTCATATCATCCCTGCGTAC		748
D	731	actctacatcaaaagcgaacgcgctctctcaacaataattcatctatctcttggctg		790
D	749	TCAATCACTGCTGGCCATCTCTGTCTTACCTTGCCCTCAGACTGTGATGAAATAATTA		808
D	791	tcatcaactctgtctatctctgtctcttcaactgacctccgcagactgaggagaaatga		850
D	809	CATTTTGTATTTCTGTGGTGTGTAGACACTACAGATTTCTCTCTCATATCTCCAAATTG		868
D	851	cgcctcgcactctctgtctgtcgtgacactcaagctctctcctgtcgtcatctccaagatcg		910
D	869	TGCGTCCCACTCCCTCATATTCACCGTGGTGGGCAAGACCTCATTTTATCATGTGTC		928
D	911	tgcctcccaactccctctgacatacagcgtcatcttgcaagtaacctctgttcaacatgctgc		970
D	929	TATTCACCTTTTCCATTCGTACACAGGCTGTGTGTGTCAATGTGACACACGGTGGCTTA		988
D	971	tgttcaactcttccatctgtacacacatggtgtgtctctaaatgtagacacacgctcaacca		1030
D	989	CCACGACACATATGGCCCGCTGGGTGTAAAGTGTCTTCTGTGGAACAAATGCCCACTTCG		1048
D	1031	gactcaacacacatggaatctcgggttcaaggaagtgctctccctgcacaaacatgcacactctc		1096
D	1049	TCTTCTCTGACGACGACCCACCGCCATGCTGTGCATGCTCCGCTTGAAGAGCGGCC		1108
D	1091	tctctctgaagatgcctcgggtcttgaagtcagcgtctcaaggtctccatcccaagcagc		1150
D	1109	AGCGACAGCGTGAAGGCGCAGCGGGTTTCTCCGTGAAGGCTCTGCGGCTGACCCATGTA		1168
D	1151	tgcactctgcccacagctgatactctgcagcaactctgtcctttagcaccacaagactca		1210
D	1169	CTGTGTTTGTGCA-----AACCTGCATCATGCTCAAGGCGTTGAG		1204
D	1211	acctcatcttgaggtatcctcaatctgtatgtaaacctgtctccgtccgcgtccctcaatctgcag		1270
D	1205	CTTGGGCTTTTCGAGACTTACGCCCACTGCACACGGCCCGGGCGCTGTGTGGGCGCATGGA		1264
D	1271	tcagctcccaacacagcagcgctcccccaggaatgcccgtctgaggtctctccggaggttcc		1330
D	1265	GCATGTGGCTCCGGGAGACCAATGTGATGGCGTATGCGTCAATTGGCGGACACATATCGAATGG		1324
D	1331	gggaagaatctaaagaagcatctagaggtgtcatctatctaccacagcatctgtgagaagc		1390
D	1325	AGGATGATATACCAAGAGTGTGAAGGAGAGCATGGAATAACTGTTCCTCATGTATGACACGCC		1384
D	1391	atgacccgaatcaaaagtgtctatcgaagacatggaaatctcgtgcgaatggtgtgtgacagcc		1450
D	1385	TGTTCCTGTGATCTTTGTCTTGTCTTGTCTGTCTCTTGTGGAGACCGTGGCATGTTTCTTGACG		1444

[illegible]







PA (UNBO-) UNIV BONN.  
 PA (UNIV) UNIV MELBOURNE.  
 PA (WOMEN-) WOMEN'S & CHILDREN'S HOSPITAL.  
 XX Berkovic SF, Mulley JC, Phillips HA, Propping PJ;  
 PI Scheffer IE, Steinleink, Sutherland GR, Wallace RH;  
 XX WPI: 1997-100506/10.  
 DR P-PSDB: AAM11824.  
 XX  
 XX CHRNA4 gene encodes neuronal nicotinic acetylcholine receptor  
 PT fragment - used in diagnosis of autosomal dominant nocturnal frontal  
 PT lobe epilepsy  
 PS  
 PS Claim 5; Fig 13; 20pp: English.  
 CC The DNA sequence of the normal nAChR is given in AAT59527,  
 CC the DNA sequence of the ADNFLE-inducing mutant is given in AAT59528.  
 CC Mutations at codon 248, which have the effect of replacing  
 CC serine by another amino acid (e.g. phenylalanine) in the sixth  
 CC amino acid of the transmembrane domain 2 (M2) of the alpha  
 CC subunit of nAChR have been found to be associated with ADNFLE.  
 CC The primers given in AAT59529 and AAT59530 were used in the  
 CC amplification of part of exon 5.  
 CC  
 XX  
 SQ Sequence 2082 BP; 367 A; 768 C; 592 G; 355 T; 0 other;

Query Match 28.7%; Score 434.2; DB 18; Length 2082;  
 Best Local Similarity 65.7%; Pred. No. 4e-104;  
 Matches 657; Conservative 0; Mismatches 313; Indels 15; Gaps 2;

QY 89 ACACAGAGCGGCTAGTACATCTCTTATGATCCCTCCGATTAACAGCTGATTC 148  
 DB 282 agccgagagagcgccctcgaagaacctc-----cccggtacacagcggtcc 335  
 QY 149 GTCCAGCTACTAACGCGCTGAGCTGAGCTGATACAGCTGATGATTCGCTCAGC 208  
 DB 336 gaccctgagcacaatctcgaagctcgtccgtccgtccgtccgtccgtccgtcc 395  
 QY 208 TCATTAGTGTGACAGAGCGGAGAGATGATGACACCAATGCTGCTGACCCAGAGT 268  
 DB 396 tcaattgacgtgagatgagagacacagatgagacagatgagatgagatgagatg 455  
 QY 269 GGCAGATTACCGCTCAGATGAGAGCGTGAAGCTTGCACATGTAAGAAGTCCGGC 328  
 DB 456 ggcagactacaaagctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 515  
 QY 329 TCCCTTCAACACATGCTGCTCCAGATGTGCTTATACAAATGCTTACCGCATGT 388  
 DB 516 tccctcgcagatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 575  
 QY 389 ACGAGTCTCTTCTATTCATGCTGTGCTCTCTATGATGAGCATCTTTGGCTAC 448  
 DB 576 tgcggtac 635  
 QY 449 CACCTGCATCTACAGAGTGCATGAGATGAGATGAGATGAGATGAGATGAGATG 508  
 DB 636 ccccgcatctacaaagctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 695  
 QY 509 AGAATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 568  
 DB 696 agaaactgac 755  
 QY 569 TCNAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 628  
 DB 756 acatgac 815  
 QY 629 CACTGCCAGCGCAGACAGAGACCCAGACACTCC-----ACCTATGAGACA 679  
 DB 816 atgcgctgagcaccac 875  
 QY 680 TCACCTATGATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 739

DB 876 tcacctatgctcctcgaac 935  
 QY 740 CCGGCTGATCATCATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799  
 DB 936 cctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 995  
 QY 800 AAAAGATGACACTTTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859  
 DB 996 agaaatgac 1055  
 QY 860 CCAAGATTTGCTCCTCCAGCTGATGATGATGATGATGATGATGATGATGATGATG 919  
 DB 1056 ccgagatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1115  
 QY 920 CCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 979  
 DB 1116 ccatgactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1175  
 QY 980 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039  
 DB 1176 gctgcac 1235  
 QY 1040 CCACCTGCTCTCTCTCTGACAGACCC 1064  
 DB 1236 caagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1260

## RESULT 11

AAT48237  
 ID AAT48237 standard; DNA; 3496 BP.  
 XX  
 XX AAT48237:  
 DT 09-APR-1997 (first entry)  
 XX  
 DE Neuronal nicotinic acetylcholine receptor alpha-4 subunit DNA.  
 XX  
 KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;  
 KW ligand-gated receptor; ds.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 232..2115 /tag= a  
 FT CDS misc\_difference 3344 /tag= b  
 FT /note= "base 3344 is given as n in the  
 FT specification"  
 FT  
 FN W09641876-A1.  
 FN  
 PD 27-DEC-1996.  
 PD  
 XX  
 XX 07-JUN-1996; 96MO-US09775.  
 PF  
 XX  
 XX 07-JUN-1995; 95US-0484722.  
 PR  
 XX  
 XX (SIBI-) SIBIA NEUROSCIENCES INC.  
 PA  
 PA Elliott KJ, Harpold MM;  
 PI WPI: 1997-065463/06.  
 DR P-PSDB: AAM09023.  
 DR  
 XX  
 XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -  
 PT used in screening to determine the effect of drugs on the receptor  
 PT  
 XX  
 XX Disclosure: Page 58-61; 108pp; English.  
 CC A DNA sequence (AAT48237) codes for the alpha-4 subunit (AAM09023) of  
 CC the human neuronal nicotinic acetylcholine receptor (nAChR). Host



QY 89 ACACAGAGAGGCGGTAGTGGACATCTTTAGATCCCTCCCGGTATACAGAGTATC 148  
 DB 282 acgcgagagagcgctctctgaaagaactct-----ctccggttacacaagtggtccc 335  
 QY 149 GTCCAGCTACTATACGGCTGAGCTGTGACTGATACAGTCAATGATCATTTGCTACGC 208  
 DB 336 gaccgctggcacaacatctcgagagctcgtccgtctcgtccgtccgtccgtccgtccgc 395  
 QY 209 TCATTAGTGTGCACGAGCGGAGCATCATGACCAACAATGTGCGTGAACCCAGAGT 268  
 DB 396 tcatgacgctgagagaaacacagatgacacagacgtatgagtgagagagagt 455  
 QY 269 GGGAAATTAACCGCTCATCATGGAAGCGTGAAGTTCGACATATGAGAAGTCCGCGC 328  
 DB 456 ggcacagactaaagaactcgcgtggagcccgctgacatgagatgacacccatccgcga 515  
 QY 329 TCCCTTCCAAACATCTGGCTCCAGATGTGTTCTATACAAATGCTGACGCATGT 388  
 DB 516 tccctcgcgactcatctcgtcgccgagactcgtctcctacacaaatgctgagcgagact 575  
 QY 389 AGCAGTCTCTCTTATTCATGCTGTGTGTCCTCATATGATGGACGATCTTTGGCTAC 448  
 DB 576 tctggtgctacccaccctgacaaagccaccctgacatgacgagcgagtcgaagtgagctc 635  
 QY 449 CACCTGCTATATACAGATGTCATGCAAGAATGAGTGAAGCATCTCCATTTGACGAGC 508  
 DB 636 ccccgccatltacaaagagctcctgacagatcgcagctctcctccctcgcagcagc 695  
 QY 509 AGAATTCACACCATGAGTTCGCTCATGACGTCAGACCGTATGAGTGAATGATGCTGTCG 568  
 DB 696 agaactgcacatgaaatctcgctcctgacatgacaaagccaaagtcgacactggtga 755  
 QY 569 TCAAAAGATGATGTCGACGATGATGATGATGATGATGATGATGATGATGATGATG 628  
 DB 756 acatgcacagacgctgagacgactgagactctgagagagtgagtgagtgagtgagtgag 815  
 QY 629 CACTGCCAGCGCCAGCAGAGAGACCCAGAGACTCC-----ACCTATGTGACA 679  
 DB 816 atgcgctggagacatcaacacagaaagatgacgagtgctgacgagtgacacccgagaca 875  
 QY 680 TCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 739  
 DB 876 tcaactaagctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 935  
 QY 740 CCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 799  
 DB 936 cctgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 995  
 QY 800 AAAAGATGACACTTGTATTTGTGCTGCTAGCACTACAGGTCGTCGTCGTCGTCGTCGTC 859  
 DB 996 agaagatcaacgctgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1055  
 QY 860 CCAAGATTGTGCTCCCACTCCCGATGATGACCGTGTGAGGAGTGAAGTGAAGTGAAGT 919  
 DB 1096 cccgagatcaatccgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1115  
 QY 920 CCATGCTGCTAGTACCTTCTCATGCTGCTACCAAGCTGTGTGTGCTCATGTCGACAC 979  
 DB 1116 ccaagatcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1175  
 QY 980 CCTGCTGCTACGACGACACCAAGGCGCCCTGAGTCAAGGTCGTCGTCGTCGTCGTCGTC 1039  
 DB 1176 gctcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1199  
 QY 1040 CCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064  
 DB 1236 cagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1260

RESULT 13  
 AAV12196  
 ID AAV12196 standard: cDNA; 2363 BP.  
 XX

AC AAV12196;  
 XX 14-MAY-1998 (first entry)  
 DT Human neuronal nicotinic acetylcholine receptor alpha-4 subunit cDNA.  
 DE Human neuronal nicotinic acetylcholine receptor; alpha-4 subunit;  
 KW Human; neuronal nicotinic acetylcholine receptor; alpha-4 subunit;  
 RW brain tissue; screening; NACHR; antibody; ds.  
 XX Homo sapiens.  
 OS  
 FT Key Location/Qualifiers  
 FT CDS 173..2056  
 FT /tag=a  
 FT /product="neuronal nicotinic acetylcholine receptor  
 alpha-4 subunit"  
 PD MO9420617-A2.  
 PD 15-SEP-1994.  
 PD 08-MAR-1994. 94MO-US02447.  
 PD 08-MAR-1993. 93US-0028031.  
 PR (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 PA (SIBI-) SIBIA NEUROSCIENCES INC.  
 XX Elliott KJ, Ellis SB, Harpold MW;  
 XX WPI: 1994-303024/37.  
 DR P-PSDB; AAM44152.  
 XX  
 PT Human neuronal nicotinic acetylcholine receptor subunits and DNA -  
 PT also transformed cells useful for screening cpds. which modulate  
 PT activity of the receptor  
 XX  
 PS Claim 4: Page 74-75; 99pp; English.  
 CC The present sequence encodes a human neuronal nicotinic acetylcholine  
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta  
 CC NACHR subunits may be used in a method of screening compounds to  
 CC identify any which modulate the activity of human neuronal NACHR.  
 CC Subunit specific antibodies may be used to monitor the distribution  
 CC and expression density of various subunits in normal vs diseased brain  
 CC tissues. Testing of single receptor subunits or specific receptor  
 CC subunit combinations with a variety of potential agonists or antagonists  
 CC provides information with respect to the function and activity of the  
 CC individual subunits and should lead to the identification and design of  
 CC compounds that are capable of very specific interaction with one or  
 CC more receptor subtypes. The resulting drugs should exhibit fewer  
 CC unwanted side effects than drugs identified e.g. screening with cells  
 CC that express a variety of subtypes.  
 XX  
 SQ Sequence 2363 BP; 397 A; 861 C; 696 G; 403 T; 6 other:  
 Query Match 27.8%; Score 419.8; DB 15; Length 2363;  
 Best Local Similarity 65.8%; Pred. No. 2.5e-100;  
 Matches 648; Conservative 0; Mismatches 322; Indels 15; Gaps 2;  
 QY 89 ACACAGAGAGGCGGTAGTGGACATCTTTAGATCCCTCCCGGTATACAGAGTATC 148  
 DB 276 acgcgagagagcgctctctgaaagaactct-----ctccggttacacaagtggtccc 329  
 QY 149 GTCCAGCTACTATACGGCTGAGCTGTGACTGATACAGTCAATGATCATTTGCTACGC 208  
 DB 330 gaccgctggcacaacatctcgagagctcgtccgtctcgtccgtccgtccgtccgtccgc 389  
 QY 209 TCATTAGTGTGCACGAGCGGAGCATCATGACCAACAATGTCGCTGAACCCAGAGT 268  
 DB 390 tcatgacgctgagagaaacacagatgacacagacgtatgagtgagagagagt 449











GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 03:04:22 ; Search time 1878.98 Seconds

(without alignments)  
11890.780 Million cell updates/sec

Title: US-07-938-154-10

Sequence: 1 ATGCTGGCTGTGATGGCCGG.....CAGCTCCAGCTCCAGTGA 1512

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1415048 seqs, 738405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending Patents NA Main: \*  
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4: /cgn2\_6/ptodata/2/pna/US08.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/pna/US081.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/pna/US082.COMB.seq: \*  
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8: /cgn2\_6/ptodata/2/pna/US084.COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1159	76.7	2448	US-08-487-596-13	Sequence 13, Appl
2	1159	76.7	2448	US-08-660-451A-13	Sequence 11, Appl
3	1159	76.7	2450	US-08-028-031-9	Sequence 9, Appl
4	1159	76.7	2450	US-09-217-345-9	Sequence 9, Appl
5	1159	76.7	2450	US-06-245-225-514	Sequence 514, Appl
6	1159	76.7	2450	US-06-258-250-154	Sequence 154, Appl
7	1157	76.3	1309	PCT-US01-10666-2	Sequence 2, Appl
8	1154.8	76.4	1633	US-06-248-505-1732	Sequence 1732, Ap
9	1094.8	72.4	1605	US-06-248-505-1455	Sequence 1455, Ap
10	881	58.3	1633	US-06-230-445-2311	Sequence 2311, Ap
11	739.4	48.9	11942	PCT-US01-10666-126	Sequence 126, Appl
12	738.2	48.8	11083	US-06-230-445-277	Sequence 277, Appl
13	738.2	48.8	11942	PCT-US01-10666-1	Sequence 1, Appl
14	738.2	48.8	1826	US-06-245-225-44	Sequence 44, Appl
15	738.2	48.8	1826	US-06-258-250-14	Sequence 14, Appl
16	738.2	48.8	13083	US-06-248-505-400	Sequence 400, Appl
17	738.2	48.8	17808	US-06-248-505-123	Sequence 123, Appl
18	712.8	47.1	1962	US-06-207-214-38	Sequence 38, Appl
19	712.8	47.1	2834	US-06-207-214-122	Sequence 122, Appl
20	712.8	47.1	2834	US-06-207-214-123	Sequence 123, Appl
21	712.8	47.1	2834	US-06-207-214-124	Sequence 124, Appl
22	693.4	45.9	1915	US-08-487-596-17	Sequence 17, Appl
23	693.4	45.8	1915	US-08-660-451A-17	Sequence 17, Appl
24	688.6	45.5	1915	US-08-028-031-11	Sequence 11, Appl
25	688.6	45.5	1915	US-09-217-345-11	Sequence 11, Appl
26	496	32.8	743	US-06-178-306-22	Sequence 22, Appl
27	496	32.8	743	US-06-178-306-23	Sequence 23, Appl
28	496	32.8	743	US-06-178-306-24	Sequence 24, Appl
29	496	32.8	743	US-06-178-306-25	Sequence 25, Appl
30	496	32.8	743	US-06-178-306-26	Sequence 26, Appl
31	496	32.8	743	US-06-178-306-27	Sequence 27, Appl
32	496	32.8	743	US-06-178-306-28	Sequence 28, Appl
33	496	32.8	743	US-06-178-306-29	Sequence 29, Appl
34	496	32.8	743	US-06-178-306-30	Sequence 30, Appl
35	496	32.8	743	US-06-178-308-34	Sequence 34, Appl
36	496	32.8	743	US-06-178-308-35	Sequence 35, Appl
37	496	32.8	743	US-06-178-308-36	Sequence 36, Appl
38	496	32.8	743	US-06-178-308-37	Sequence 37, Appl
39	496	32.8	743	US-06-178-308-1503	Sequence 1503, Ap
40	482.8	31.9	671	US-06-178-306-302	Sequence 302, Appl
41	482.8	31.9	671	US-06-178-306-632	Sequence 632, Appl
42	464.4	30.7	699	US-06-178-306-174	Sequence 174, Appl
43	464.4	30.7	699	US-06-178-306-175	Sequence 175, Appl
44	464.4	30.7	699	US-06-178-306-176	Sequence 176, Appl
45	464.4	30.7	699	US-06-178-306-177	Sequence 177, Appl





QY	788	CAGATGTGGTGAAGAAAGTATGACACTTTTGATTTCTGTGACGTACAGACTTCACGGTGTTC	847
Db	1043	CCGACTGTGGCAGGAAGATATACGTGTGTGATATCAGTGTCTGTCTGACGGCTCACGGTCTTCC	11024
QY	848	TGCTGTCTATCTCCAAAGATTGTGTGCTTCCACCTCCCTCGATGTACGTACGCTGTGTGGGCAAGT	907
Db	1103	TGCTGTCTATCTCCAAAGATTGTGTGCTTCCACCTCCCTCGATGTACGTACGCTGTGTGGGCAAGT	11624
QY	908	ACCTCATGTTTAAACATGGATGGTGTATCCACCTTCCTCATCGACACAGCTGTGTGTCTCA	967
Db	1163	ACCTCATGTTTAAACATGGATGGTGTATCCACCTTCCTCATCGACACAGCTGTGTGTCTCA	12224
QY	968	ATGTGCACACACCGCTGTGCTTACACACGACACCATATGGCCCGCTGGGTCAAGGTGGTCTTCC	1027
Db	1223	ACGTGTACACACCGCTGTGCTTACACACGACACCATATGGCCCGCTGGGTCAAGGTGGTCTTCC	12824
QY	1028	TGGGAAGGTGGCCACCGCTGTGCTTCTCTTCAGACAGCCAGCCACCGCTGTCTACAGTCTAC	1087
Db	1283	TGGGAAGGTGGCCACCGCTGTGCTTCTCTTCAGACAGCCAGCCACCGCTGTCTACAGTCTAC	13424
QY	1088	GTCGTGCGCTTGAAGAGAGGCCACGACGAGACGCTGAAGGC--GAGGCGGCTTTTCTTCCGTC	11444
Db	1343	GCTGTGCGCTTGAAGAGAGGCCACGACGAGACGCTGAAGGC--GAGGCGGCTTTTCTTCCGTC	14024
QY	1145	AAGGTCTCGGGGCTGACCCATGTACCTGCTTTGTACACCTCGATCAGTGTGAGGCGCTTGG	1204
Db	1403	AAGGCCACAGGAGGCGCGATCTGTGACAGGCTGTGTGTACGCGGCGGTGTGTGAGAGGCTTGG	14624
QY	1205	CTGGGGCTTTTCCGAGCTGAGGCCACTGTCA--GCGGGCCCGGGGGCGCTTGTGGGGCCAT	1261
Db	1463	CCGGGGCTTTTCCGAGCTGAGGCCACTGTCA--GCGGGCCCGGGGGCGCTTGTGGGGCCAT	15224
QY	1262	GCAGCTGTGGGCTCCGGGGAAGACATGTGAGGTGTACCTTCAATCGGAGACACATACGGA	1321
Db	1523	GTGGGTGTGGGCTCCGGGGAAGACATGTGAGGTGTACCTTCAATCGGAGACACATACGGA	15824
QY	1322	GTGAGGATGTATGACACAGAGTGTGAGGAGAGACTGTGAATATCGTTGTCCATGTGTATGTAC	1381
Db	1583	GGGAGGACGATGTACAGAGGCTGTGATGTGAGACTGTGAATATCGTTGTCCATGTGTATGTAC	16424
QY	1382	GGCTGTTCCTGTGTGATCTTTGTCTTGTCTGTCTGTCTTGTGGGACGCTGTGGCATGTCTCTGC	1441
Db	1643	GGCTGTTCCTGTGTGATCTTTGTCTTGTCTGTCTGTCTTGTGGGACGCTGTGGCATGTCTCTGC	17024
QY	1442	AGCCGTCTTTCAGAACTACACACTGCACATACCTTCTCTCACCCCTGACACACTCAGCTCCCA	1501
Db	1703	AGCCGTCTTTCAGAACTACACACTGCACACACCACTTCTCTCACACTGTACACTCAGCTCCCA	17624
QY	1502	GCTCCAAAGTGA 1512	
Db	1763	GCTCCAAAGTGA 1773	
RESULT 3			
US-08-028-031-9			
Sequence 9, Application US/08028031			
GENERAL INFORMATION:			
APPLICANT: Elliot, Kathryn J.			
APPLICANT: Ellis, Steven B.			
APPLICANT: Harpold, Michael M.			
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE			
RECEPIOR COMPOSITIONS AND METHODS EMPLOYING SAME			
NUMBER OF SEQUENCES: 12			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark			
STREET: 444 South Flower Street, Suite 2000			
CITY: Los Angeles			
STATE: CA			
COUNTRY: USA			
ZIP: 90071			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/028..031
FILING DATE: 19930308
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2450 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 267..1775
US-08-028-031-9

Query Match      76.7% Score 1159; DB 4; Length 2450;
Best Local Similarity   86.8%; Pred. No. 7e-278;
Matches 1112; Conservative    0; Mismatches 190; Indels    9; Gaps    3

QY  11 GCATGCGCCGGGCACCTTCACATCATGGCGCTGTTC--AGCTTCAGCCCTTCTTTGGCTGT 67
DB  265 GCATGCGCCGGGCACCTTCACATCATGGCGCTGTTC--AGCTTCAGCCCTTCTTTGGCTGT 324
QY  68 GCTCAGGAGGTTTTGGGAACACTGACACAGAGAGCGGCTAGTGAGGACATCTTGATACCTT 127
DB  325 GCTCAGGAGGTTGGGGGTACGGATACACAGAGAGCGGCTAGTGAGGACATCTTGATACCTT 384
QY  128 CCCGCTAATCAACAAGCTGATTGTCACAGCTACTAAAGGCTCTGAGCTGTACTGTACAGC 187
DB  385 CCCGCTAATCAACAAGCTTATCCGCCAGCCACCATTGGCTCTGTAGCTGGTAGCACAGTACAGC 444
QY  188 TCATGGATCATGATGGCTCAGCTCATTAATGTTGACAGAGGAGGAGGAGCATCATACACACA 247
DB  445 TTAATGTGTACAGTGGCCAGGCTCATCAGTGTGTACATGAGCGGAGAGCATATACACACA 504
QY  248 ATGTCGTGCTGACCCAGAGAGTGGGAAGATTACCCCTTCACATGAGAAGCTGAGAGACTCG 307
DB  505 ATGTCGTGCTGACCCAGAGAGTGGGAAGATTATCCCTTCACATGAGAAGCTGAGAGATTGG 564
QY  308 ACAATATGAGAAAGTCGCGGCTCCCTTCCAACAACATCTGGCTCCCAAGATGTGGTCTAT 367
DB  565 ACAACATGAGAAAGTTGGGCTCCCTTCCAACAACATCTGGCTCCCAAGATGTGGTCTAT 624
QY  368 ACACAAATGCTGACGGCATGTAGCAAGTCTCCTTTATTTCAATGCTGTGGTCTTCATG 427
DB  625 ACACAAATGCTGACGGCATGTAGCAAGTCTCCTTTATTTCAATGCTGTGGTCTTCATG 684
QY  428 ATGGACACATCTTTGGCTACACACCTGCACTCTCAAGAGTGCATGCAAAATTTAGAGTGA 487
DB  685 ATGGACACATCTTTGGCTGCGCGCTGCCATCTCAAGAGAGGCGCATGAAATTTAGAGTGA 744
QY  488 AACACATCCCATTTTGAACACAGACAAATTTGACCAATGAAGTTTGGCTCATGAGACTACAGC 547
DB  745 AACACATCCCATTTTGAACACAGACAAATTTGACCAATGAAGTTTGGCTCATGAGACTACAGC 804
QY  548 GTACTGAGATTTGACCTGGTGGCTCAAAGAGATGTGGCGAGTGTGGATGATTTACACCCA 607
DB  805 GCACGAGAGATCACTTGGTGTGTGAAGAGTGAAGTGGGCGACGCTGTGAGAGACTTACACCTA 864
QY  608 GCGGGAGATGGGACATCATGCACTCCAGGCGGACGACGAAGAACCCAGACACTCCA 667
DB  864 GCGGGAGATGGGACATCATGCACTCCAGGCGGACGACGAAGAACCCAGACACTCCA 924

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Dg	865	GTGGTGAAGTGGGACATCGTGGCCCTCGGGGCGGACGACGAAACGCCGAGACTCTA	924
Qy	668	CCATATGGACATCACTTATAGCTTATCATTTGTGCGAAMACCACTCTTTACATCTA	727
Db	925	CGTACGTGGACATCACTATAGCATTTTCATTTGCGCGAAGCCGCTCTTTACACATCA	984
Qy	728	ACCTATATCCCTCCGGTATCATACCTCCGCTGGACATCTGGTCTTTTACCTCCCT	787
Db	985	ACCTATATCCCTCCGGTATCATACCTCCGCTAGCATCTTTGTCTTACCTGCAT	1044
Qy	788	CACATGTGTGGAAAAGTATGACCTTTGTATTTTGTGTCTGTAGCACTACGATGTTC	847
Db	1045	CGACATGTGTGGAAAGTATGACCTTTGTATTTTGTGTCTGTAGCACTACGATGTTC	1104
Qy	848	TGCTGTATCTCCCAAGTTGTGCTCCCACTCCCTCGATGTACGCTGTGGGCAAT	907
Db	1105	TGCTGTATCTCCCAAGTTGTGCTCCCACTCCCTCGATGTACGCTGTGGGCAAT	1166
Qy	908	ACCTCATTTTACATGTGTCTATGATCACTTCTCATGTGTACCAAGCTGTGTCTCA	967
Db	1165	ACCTCATTTTACATGTGTCTATGATCACTTCTCATGTGTACCAAGCTGTGTCTCA	1224
Qy	968	ATGTGCACACACCGCTCGCTATACACAGCACACANTGACCCCTGTGGTCAAGGTGTTCC	1021
Db	1225	ACGTGCACACACCGCTCGCTATACACAGCACACANTGACCCCTGTGGTCAAGGTGTTCC	1284
Qy	1028	TGAGAGAAGCTGGCCACCCCTGCTCTCTCTGACAGACACAGCACAGCTGTGTACAC	1087
Db	1285	TGAGAGAAGCTGGCCACCCCTGCTCTCTCTGACAGACACAGCACAGCTGTGTACAC	1344
Qy	1088	GTTGTGGCTTGAAGAGGCGGACGAGAGAGGTGAGAGGC--GAGGCGGTTTTCTTCGAG	1144
Db	1345	GCTGTGGCTTGAAGAGGCGGACGAGAGAGGTGAGAGGCCTTCTTCGCGG	1404
Qy	1145	AAGGTCTCGCGGTATACCATATGATACGCTTTGTATCAACCTGTACATGATGACAGCTTGG	1204
Db	1405	AAGGTCTCGCGGTATACCATATGATACGCTTTGTATCAACCTGTGTGATGAGGTTGG	1466
Qy	1205	CTTGGGCTTTCGGAAGCTTATGAGCCACTGTCA---GCGGCGCGGGGCGCTCTGTGGGCAAT	1261
Db	1465	CGGGGCTTTCGGGCTTATGAGCTTGCACACATGTGGCGGGGCCCGGGGCTCAAGGGAACCGT	1524
Qy	1262	GCAAGTGTGGCTCCGGGAAGACAGTGTATGGCGTATGCTTATTTGCGAGACACATGCGAA	1321
Db	1525	GTTGGCTGTGGCTCCGGGAAGACAGTGTATGGCGTATGCTTATTTGCGAGACACATGCGGA	1584
Qy	1322	GTTGAGATATATACAGAGATGTGAGGAGAGACTGTGAAATATGCTTGTCCATGGTATGAGAC	1381
Db	1585	GCGAGAGCATATACAGAGAGCTGTAGATGAGACTGTGAAATATGCTTGTCCATGGTATGAGAC	1644
Qy	1382	GCGTGTCTGTGAGATCTTTTCTTTTCTGTGTCTTTTGTGAGACGCTGGGATGTTCTCG	1441
Db	1445	GCGTGTCTGTGAGATCTTTTCTTTTCTGTGTCTTTTGTGAGACGCTGGGATGTTCTCG	1704
Qy	1442	AGGCTCTTTCCAGAAATACACCTCCACTCTCTCTCTCCACCGCTGACACATCAAGCTGCCA	1501
Db	1705	AGGCTCTTTCCAGAAATACACCTCCACTCTCTCTCTCCACCGCTGACACATCAAGCTGCCA	1766
Qy	1502	GCTTCCAAAGTGA 1512	
Db	1765	GCTTCCAAAGTGA 1775	
RESULT 4			
US-09-217-345-9			
Sequence 9 Application US/09217345			
GENERAL INFORMATION:			
APPLICANT: Ellis, Kathryn J.			
APPLICANT: Ellis, Steven B.			
APPLICANT: Harpold, Michael M.			
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE			
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME			
NUMBER OF SEQUENCES: 12			

OY	368	ICAAACATGCTAGAGGCAATGAGAGAGTGCCTCTTATATTCATATGCTGGGCTCCATAG	427
Db	625	ACAAACATGCTAGAGGCAATGAGAGAGTGCCTCTTATATTCATATGCGGTCTCTCATAG	684
OY	428	ATGGCAAGCATCTTCTTGGCTACACACAGCCGATCTCTTCAAGAGTGAATGACAAATGAGTGA	487
Db	665	ATGGCAAGCATCTTCTTGGCTACCGCTGCGCTCGCATCTTACACAGCGATGACAAAGTAAATGA	744
OY	488	AGCACTTCCCATTTGATGACAGAGAAATATGACATGAAGTTGGCTCTATGAGCATCTAGACC	547
Db	745	AGCACTTCCCATTTGATGACAGAGAACTGACACATGAAGTTGGCTCTATGAGCATCTAGACC	804
OY	548	GTACTGATTAATCTAGTGTGCTCAAAAATGATATGTCGCAATGTCGATGATCTTACACCCA	607
Db	805	GCACAGAGATTCACATGGTGTGTAAAGAGAGAGTGGCACCTCTGACAGATTCACACCTA	864
OY	608	CGGGGAGTGGACATCATCCGACCTGCGACGCGGACGACGAAACCCAGACACATCCA	667
Db	865	GTGGTATGAGGGAGACATCCGTGGCCCTCTCGGGGCGGGCAACGAGAAACCCGACACACTTA	924
OY	668	CCATATGTGACATCCACCTATGACTTATCATATCTTGCACAAACCACTCTTCTACACTATCA	727
Db	925	CGTACGTGGACATCCACGTATGACTTATCATATCTTGCACAAACCGGCTCTTCTACACTATCA	984
OY	728	ACCTCATATATCCCTGCGCTACATCATACCTGCGTGGGCATCTCGGCTCTTCTACCTGACCC	787
Db	985	ACCTCATATATCCCTGCTGTGCTCATCATCCCTGATAGCAATCTCTTGTCTTCTACCTGGCAN	1044
OY	788	CAGACGTGTGTAAAGATGACATCTTGTATTTGTGTGTGCTGTAGACATCCAGCTGTGTCC	847
Db	1045	CCGACGTGTGTGAGAAAGATGACATCTTGTGATCTCATAGTGTGTGTGGGGGTCAACGGTCTTCC	1104
OY	848	TGCTGCGCATCTCCCAAGATGTGTGTGCTCCGACCTCCCGCATGATGACCGTGTGTGGGCAAG	907
Db	1105	TGCTGCGCATCTCCCAAGATGTGTGTGCTCCGACCTCCCGCATGATGACCGTGTGTGGGCAAG	1164
OY	908	ACCTCATATGTTTACATATGCTGTAGTACCTCTCTCATCTGTACATCCACAGCTGTGTGTGTGA	967
Db	1165	ACCTCATATGTTTACATATGCTGT	1224
OY	968	ATGTGACACACCGCTGCGCTACACACGACACACACATGAGCCGCTGTGGTCAAGTGGTCTTCC	1027
Db	1225	ACGTGACACACCGCTGCGCTGCGCACACACACACATGAGCCGCTGTGGTCAAGTGGTCTTCC	1284
OY	1028	TGAGAACTGTCCCAACCTGCTCTTCTCTGACAGACCCACGCGCATGTGTGCACATGTAC	1087
Db	1285	TGAGAACTGTCCCGCTGCTCTTCTTATGTACAGAGCCACGCACTCATATTTGGCCCGCTGTAC	1344
OY	1088	GTTCTGCGCTTGAAGAGGGGCCACAGAGAGCGTGAAGGC -- -GAGCGGGTTTTTCTTCGTTG	1144
Db	1345	GCTCTGCGCTTGAAGAGGGGCCACAGAGAGCGCGAGGCGCGTGTAGACCTCTTCTTCCGCGG	1400
OY	1145	AAGGTCCTTGGCGCTGACCAATGATACCTGTCTTGTTCACACCTGTCATCACTGTGAGAGCGTTG	1204
Db	1405	AAGGTCCTTGGCGCTGACCACTCTGTCACATGTCTTGTTCACACCGCGTGTGTCAGAGGGTTGG	1464
OY	1205	CTGGGGCTTTTCCGAGGTGAGCCCACTGCA -- -GCGGCGCGGGGGGCGTCTGTGGGCGCAT	1261
Db	1465	CTGGGGGCTTTTCCGAGGTGAGCTGCACTGCAAGAGTGGGCGCGCGGGGGCGTCAAGGGAGCCGT	1524
OY	1262	GCACGTGTGGGCTCGGGGAGACAGTGAATGAGCTGTACCTCTTCAATGTGCGGACCACTATGGA	1321
Db	1525	GTGGGTGTGGCTCGGGGAGGCGTGTGAAGCGCGTGTGCTTCAATGCCACACATGTGGA	1584
OY	1322	GTGAGGATATGACCAAGTGTGAGGAGGAGCACTGGAATATGCTGTGCGCATATGCTGTATGTAGC	1381
Db	1585	GCAGAGACATATGACCAAGTGTGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	1644
OY	1382	GCGTGTCTCTGTGTGATCTTGTGTCTTGTGTCTGTGTCTTGTGGACGCTGTGGCATGTCTCTCG	1441
Db	1645	GCGTGTCTCTGTGTGATCTTGT	1704
OY	1442	AGCCTCTCTTCAGAACTACATGCTGCACACTTCTCTCCACCTGTACCACTCACTCACTCACTCA	1501

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Db      1705  AGCGCTGTTTCAGAAACTACACCAACCACTTCCCTCAGCTACAGACCTCAGCCCCA   1764
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OY      1502  GCTCCAGACTGA   1512
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Db      1765  GCTCCAGACTGA   1775

RESULT          5
US-60-245-225-514
? Sequence 514, Application us/60245225
? GENERAL INFORMATION:
? APPLICANT: Beasley, Ellen
? TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
? TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
? TITLE OF INVENTION: PROTEINS, AND USES THEREOF
? FILE REFERENCE: CLO00885
? CURRENT APPLICATION NUMBER: US/60/245,225
? CURRENT FILING DATE: 2000-11-03
? NUMBER OF SEQ ID NOS: 705
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 514
? LENGTH: 2450
? TYPE: DNA
? ORGANISM: Human
? US-60-245-225-514
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[illegible]



Db 1105 tgcgtcctacatcccaagatcgtgctcccaactccctcagacgtgctgctgcgaagt 1164  
 QY 908 ACCTCATGTTTACCATGATGCTAGTACACTTCTGCATGCTACACAGAGTGTGTCTCA 967  
 Db 1165 accctatgctacacatgctgctgctcctccctccacatgctcaccagagtgctgctca 1224  
 QY 968 ATGTGCACACACCGTCCGCTACACACGACATGCGCCCTGGGTCAAGTGTCTTCC 1027  
 Db 1225 acgtgacacacacgctcgcctcaccacacacacacacacacacacacacacacacac 1284  
 QY 1028 TGGAGAGCTGCTCCACCTGCTTCTTCTGACAGACGACGACGACGACGACGACGAC 1087  
 Db 1285 tggagaaagctgctcgcctcctcctcctcctcctcctcctcctcctcctcctcctc 1344  
 QY 1088 GTTGGCGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1144  
 Db 1345 gctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1404  
 QY 1145 AAGCTCTGCGGCTGACCCATGTAACCTGTTTCAACCTGCAATGACGACGACGACG 1204  
 Db 1405 aagcccaagagggcgcac 1464  
 QY 1205 CTGGAGCTTTCGAGCTGACCTGACCTGCA--GCGGCGCGGCGCGCTGCGGCGCAT 1261  
 Db 1465 cggagggcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1524  
 QY 1262 GCACCTGTGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1321  
 Db 1525 gctgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1584  
 QY 1322 GTGAGATGATGACACAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1381  
 Db 1585 gcgagagagctgacacagagctgagtgagagctgagagagctgagagagctgagag 1644  
 QY 1382 GCCCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1441  
 Db 1645 gctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1704  
 QY 1442 AGCCTCTCTTCAGAACATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 1501  
 Db 1705 agcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1764  
 QY 1502 GCTCCAGTGA 1512  
 Db 1765 gctccaaagctga 1775

RESULT 7  
 PCT-US01-10666-2  
 : Sequence 2, Application PC/TUS0110666  
 : GENERAL INFORMATION:  
 : APPLICANT: Genaisance Pharmaceuticals, Inc.  
 : APPLICANT: Choi, Julie Y.  
 : APPLICANT: Klem, Stefanie C.  
 : APPLICANT: Koshy, Beena  
 : APPLICANT: Lee, Helen H.  
 : APPLICANT: Sanchis, Angela  
 : TITLE OF INVENTION: HAPLOTYPES OF THE CHRN2 GENE  
 : FILE REFERENCE: MMH-0301PCT CHRN2  
 : CURRENT APPLICATION NUMBER: PCT/US01/10666  
 : PRIOR FILING DATE: 2001-04-03  
 : PRIOR APPLICATION NUMBER: 60/194,155  
 : PRIOR FILING DATE: 2000-04-03  
 : PRIOR APPLICATION NUMBER: 60/217,952  
 : PRIOR FILING DATE: 2000-07-13  
 : NUMBER OF SEQ ID NOS: 126  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO: 2  
 : LENGTH: 1509  
 : TYPE: DNA  
 : ORGANISM: Homo sapien  
 PCT-US01-10666-2

Query Match 76.5% Score 1157; DB 1; Length 1509;  
 Best Local Similarity 86.8% Pred. No. 1, 9e-277;  
 Matches 1310; Conservative 0; Mismatches 190; Indels 9; Gaps 3;

QY 13 ATGGCGGGGCACTCCAACTCAATGCGCTGTC--AGCTTCAAGCTTCTTGGCTGTGC 69  
 Db 1 atggccggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 60  
 QY 70 TCAGGAGTTTGGAGACATGACACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 129  
 Db 61 tcaggagtggtgagacagatgacagagagagagagagagagagagagagagagagagagag 120  
 QY 130 CGCTATTAACAGCTGATTCGTCACAGCTACTAAGGCTCTAAGCTGTGATGTACAGCTC 189  
 Db 121 cgtacaacaaagcttactcgcgcacacacacacacacacacacacacacacacacacacac 180  
 QY 190 ATGGATCATTTGCTCAGCTCATTTAGTGTGACAGAGGAGGAGGAGGAGGAGGAGGAG 249  
 Db 181 atggttcaactggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 240  
 QY 250 GTCTGGCTGACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 309  
 Db 241 gctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 300  
 QY 310 AATATGAAGAAATGTCGGCTCCTCCAAACACATGCTGCTCCAGATGTGTTATAC 369  
 Db 301 aacatgaagaagctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 360  
 QY 370 AACATGCTGACGAGCATGTAGAGAGTCTCTTCTTATTCATGCTGAGGCTGATGAT 429  
 Db 361 aacatgctgacgacagatgacagagagagagagagagagagagagagagagagagagag 420  
 QY 430 GCGACATCTTTTGGCTACCACTGCTCATACAGAGTGTGATGAGTGAAG 489  
 Db 421 ggcagacatcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 480  
 QY 490 CACTTCCATTTGACAGCAGAAATGACCATGAGTTGCTGATGAGCTGACGACGCT 549  
 Db 481 cacttccatctgacag 540  
 QY 550 ACTGAGATGACCTGCTGCTCAAAAGTGTGATGAGTGTGATGATGATGATGATGATGAT 609  
 Db 541 acagagatgacatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 600  
 QY 610 GGGAGTGGGACATCATGCACTGCGAGGCGGACGACGAGAGGAGGAGGAGGAGGAGGAG 669  
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 QY 670 TATGTGACATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729  
 Db 661 tagtgagacatcagatgacatcagatcagatcagatcagatcagatcagatcagatcag 720  
 QY 730 CTCATCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789  
 Db 721 ctcatcatccctgctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 780  
 QY 790 GACTGTGTTAAAGATGAGACATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849  
 Db 781 gactgtgag 840  
 QY 850 CTGCTCATCTCAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909  
 Db 841 ctgctcatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 900  
 QY 910 CTCATGTTTACATGAGTGTAGTACCTTCTCATGCTGACAGGCTGTGCTGCTGCTGCT 969  
 Db 901 ctcatggttcaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 960  
 QY 970 GTGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1029  
 Db 961 gtgacacacgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1020

QY	1030	GAAAGGTGGCCACACCGCTGCTTCTTCGACGAGACCAAGCCACCGCTGTGACGTACGCT	1089
Db	1021	gagaagatgccgcgcgcgtgcctctcaagacgacgacccatcttgcgcccgtcaagcgc	1080
QY	1090	CTGGCGCTTGAAGAGGGGCGCCAGCGAGAGCGGTGAGGGC---GAGGGCGTTTCTTCGTTGAA	1146
Db	1081	ctgcgcctgcgagagacgacgacgctgaagcgcgaagcgcgtcgtgcagcctctcttcgcgaa	1140
QY	1147	GGTCCCTCGGGCTACCCATTTACCTTCGTTTGTCAACCTTCGATCATGTCAGAGGCTTGAGCT	1206
Db	1141	gcccgaaggccgactctccgcgtcgtcttcgtcaacgcgcgtcgcgtgcaggggttgcgc	1200
QY	1207	GGGGCTTTCCGACGTAGGACCACTGCA---GCCGGCGCCGGGGCGCTCTGTGGGGCAATGC	1263
Db	1202	ggggccttcgggagcgtgaagccttgacacgaagcgcgcgcgcgcgcgtcgaaggagagcgtgt	1260
QY	1264	AGCTGTGGCTCCGGGAGACAGTGGATGGCGTACGCTTCATTGGCGACCACTGGGAAT	1333
Db	1261	ggctcgtgcctccgcggagcgcgtgcgagcgcgtgcgcttcatacgacacacatgcgagc	1320
QY	1324	GAGCATATACACAGAGTGTGAGGAGAGGACTGGAAATAGTTGGCCATGTGATCGACAGCG	1383
Db	1321	gagagcgaatgaccagagcgtgagtgagtgagcctgaaagtacgtctgcacatggtgatgcacgc	1380
QY	1384	CTGTTCCTGTGGATCTTGTGTCTTGTCTGTGTCTTGGAGCCGTGGCATGTTCTCTCAG	1443
Db	1381	ctctctcctgcgactcttgccttgccttgccttgccttgcgacatcgcatftcctgcag	1440
QY	1444	CCGTCTTCCAGAAACATCGACATTCGATTCCTGTCCTGTCCTGCAACCTCGACACATCGACGCTCCAGC	1503
Db	1441	ccctctctccagaactacacacacacacacacccctcctccatcagacacacacacagccccagc	1500
QY	1504	TCCAAGTGA	1512
Db	1501	tccaagtga	1509

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RESULT      8
US-60-248-505-1732
; Sequence 1732, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ. ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1732
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Human
US-60-248-505-1732

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Query Match	76.4%;	Score 1154.8;	DB 56;	Length 1633;
Best Local Similarity	86.7%;	Pred. No. 6.9e-277;		
Matches 1309; Conservative	0;	Mismatches 192;	Indels 9;	Gaps 3;

[illegible][illegible]



Db 1496 ctccagttca 1505

RESULT 10  
US-60-230-445-2311  
Sequence 2311, Application US/60230445  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: C1000765  
CURRENT APPLICATION NUMBER: US/60/230,445  
CURRENT FILING DATE: 2000-09-06  
NUMBER OF SEQ ID NOS: 3051  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2311  
LENGTH: 1633  
TYPE: DNA  
ORGANISM: HUMAN  
US-60-230-445-2311

Query Match 58.3%; Score 881; DB 55; Length 1633;  
Best Local Similarity 77.1%; Pred. No. 1,1e-208;  
Matches 1099; Conservative 0; Mismatches 320; Indels 6; Gaps 2;

QY 40 CTCTTCAGCTTCAGCTTCCTTGGCTGTGCTGCTGAGGCTTTTGGAACTGACACAGAGAG 99  
DB 82 ctgtactacttctgtctgtcttcccttcgaggggtgtggtgaagatcacagaagag 141  
QY 100 CGGCTAGTGAAGATCTCTTAGATCCCTCCGCTATACAACTGATTCGTCACACTACT 159  
DB 142 cggctctgtgagatctctcgtgacccctccgctacacaaagcttalcgcgccagcacc 201  
QY 160 AACGCTCTGAGCTGTGATGTACAGCTCATGTATTCATTGGCTCAGCTATTGATGTG 219  
DB 202 aatgctctctgacccacagcgttaggggctcttcgagcgtctcttcccccagccc 261  
QY 220 CAGAGGGGAGGAGTACATGACCAACATGTCGTGCTGACCCAGAGAGGAGAAATTAAC 279  
DB 262 caccagagagcaagttgtaactgctcctctcctcattcccaagagaggaagattat 321  
QY 280 CGGCTACATGAAGCCTGAGACTTTCGACAAATGAGAAAGTCGGCTCCCTTCCAAA 339  
DB 322 cgcctcaccgtgagacctgaaggtttgaacaatgaagaagtlagagaggaagaaagc 381  
QY 340 CACATCTGGCTCCAGATGTGTTCTATACAAATGCTGACGAGGATGAGAAATTCGC 399  
DB 382 tttagtccagggctgactgtgcccattcttggaagtgcagcagctgaagagtgtcc 441  
QY 400 TTCTATTCAATGCTGTGCTCTCTATGATGAGCAGCATCTTTGGCTACACCTGCATC 459  
DB 442 ttctattccaatgtcgtgtctctctatgtagaagcatcttcgtgcgcgtccatc 501  
QY 460 TACAGAGTCAATGAGATGAGTGAAGCACTTCCATTTGACAGAGAAATTAAC 519  
DB 502 tacaagagcagatgaagatgaaagaaagcattcccttgaccagagagacgcacc 561  
QY 520 ATGAAGTTTGGCTCATGAGCTTACGACCGTACTGAGATTGACCTGGTCTCAAAATGAT 579  
DB 562 atgaagtttcgttctgtgacctgacccagacagatgacttggtgttgaagagtgag 621  
QY 580 GTGGCCAGTGTGATGATTCACACCCAGCGGAGATGGAGCATCTATCCACTGCGAGCC 639  
DB 622 gtggccagctgtgagcagatctacacctagtgtgagtggaactcgtgtgcgtccgagc 681  
QY 640 CGAGCGACAGAGAACCCAGACGACTCCACTATGTGGAATCAACCTATATCTTCAAT 699  
DB 682 cggcgcaagagaaacccgagactctacgtltagtgaaatcaagtaagtaactcatt 741  
QY 700 CGTGGAAACCACTCTTCTACATATCAACTATCATCCCTGCTGCTACTCATCACTCG 759

Db 742 cgcgcgaagcgcgtctcttctacacatcaactcatcatccctgtgtgtcatcactcg 801  
QY 760 CTGACCATCTCGTGTCTTACTACCTGACCTCAGACTGTGTAAGAAAGTACATTTGATT 819  
DB 802 ctgaccatctctgtctcttctacactgtccatctcagactgtggcgaagaatagatgtgcac 861  
QY 820 TCTGTGCTGTACACTACAGGTGTTCTGCTGCTCATCTCCAAAGATTGTGCTCCAC 879  
DB 862 tcaagtgtgtgtgctcagactcaggtcttcctgtctatctccaagaatgtgtctccacc 921  
QY 880 TCCCTCATGTACCGGTGGGAGAGTACCTCATATTACCATGTGCTGCTAGTCACTTC 939  
DB 922 tccctcagctgtgcgtctgtgtgcgaagttaactcatgttaccatgtgtgttcaacttc 981  
QY 940 TCCATGCTACACAGCGTGTGTGCTCAATGTGACACACCGCTCCGCTTACACGACAC 999  
DB 982 tcatgtctaccacagctgt 1041  
QY 1000 ATGGCCCCCTGGGTCAAGGTGATCTCTTGAGAAAGTCCACACCTGCTCTTCTCTGAG 1059  
DB 1042 atggcgcctgggtgaaaggt 1101  
QY 1060 CAGCAGACCCACCGCTGTGACGTACAGCTTCCGCTTGAGAGAGCGCCAGAGAGGCT 1119  
DB 1102 cagcagacccatcatgt 1161  
QY 1120 GAGGCG---GAGCGGATTTCTTCGTGAAAGTCTCGCGCTGACCCATGATCTGCTTT 1176  
DB 1162 gagggcgtgtgagccctctctctcgcgaagcccgagggcgagctcgcagctgtctc 1221  
QY 1177 GTCAACCTCTCAATCAAGTGAAGGCTTGGCTGGGGCTTCCGAGCTGAGCCCACTGCA 1233  
DB 1222 gtcaacccgt 1281  
QY 1234 GCGGCCCCGGGCGCTCTGTGGGACATGCACTGTGCTTCGGAGAACAGATGATGAC 1293  
DB 1282 gcggccccgggcttcaagagagccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1341  
QY 1294 GTACGCTTCAATGGGAGCCATGCGAAGTGAAGATGATGACAGAGTGTGAGGGAGGAC 1353  
DB 1342 ccatctctgcatcatgt 1401  
QY 1354 TGGAAATAGTGGCATGTGATGACACCGCTGTCTGTGATCTTTGTGTGTCT 1413  
DB 1402 tgaagtagctgtgcacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1461  
QY 1414 GTCTTGGAGCCGCGGATGCTTCTGACAGCTCTCTTCAGAAC 1458  
DB 1462 gtcttggacacatgt 1506

RESULT 11  
PCT-US01-10666-126  
Sequence 126, Application PC/TUS0110666  
GENERAL INFORMATION:  
APPLICANT: Geniasance Pharmaceuticals, Inc.  
APPLICANT: Choi, Julie Y.  
APPLICANT: Kliehm, Stefanie C.  
APPLICANT: Koshiy, Beena  
APPLICANT: Lee, Helen H.  
APPLICANT: Sanchez, Angela  
TITLE OF INVENTION: HAPLOTYPES OF THE CHRN2 GENE  
FILE REFERENCE: MMH-0301PCT CHRN2  
CURRENT APPLICATION NUMBER: PCT/US01/10666  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/194,155  
PRIOR FILING DATE: 2000-04-03  
PRIOR APPLICATION NUMBER: 60/217,952  
PRIOR FILING DATE: 2000-07-13  
NUMBER OF SEQ ID NOS: 126  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 126  
LENGTH: 11942

1	TYPE	DNA
2	ORGANISM:	Homo sapien
3	FEATURE:	
4	NAME/KEY:	unsure
5	LOCATION:	(530)
6	OTHER INFORMATION:	Nucleotide identity unknown
7	NAME/KEY:	unsure
8	LOCATION:	(1006)
9	OTHER INFORMATION:	Nucleotide identity unknown
10	NAME/KEY:	unsure
11	LOCATION:	(1146)
12	OTHER INFORMATION:	Nucleotide identity unknown
13	NAME/KEY:	allele
14	LOCATION:	(3090)
15	OTHER INFORMATION:	PS1: Polymorphic base G or A
16	NAME/KEY:	allele
17	LOCATION:	(3172)
18	OTHER INFORMATION:	PS2: Polymorphic base A or G
19	NAME/KEY:	allele
20	LOCATION:	(3226)
21	OTHER INFORMATION:	PS3: Polymorphic base G or A
22	NAME/KEY:	allele
23	LOCATION:	(3331)
24	OTHER INFORMATION:	PS4: Polymorphic base C or T
25	NAME/KEY:	allele
26	LOCATION:	(3333)
27	OTHER INFORMATION:	PS5: Polymorphic base C or T
28	NAME/KEY:	allele
29	LOCATION:	(3335)
30	OTHER INFORMATION:	PS6: Polymorphic base C or A
31	NAME/KEY:	allele
32	LOCATION:	(3582)
33	OTHER INFORMATION:	PS7: Polymorphic base A or G
34	NAME/KEY:	allele
35	LOCATION:	(3594)
36	OTHER INFORMATION:	PS8: Polymorphic base A or C
37	NAME/KEY:	unsure
38	LOCATION:	(3829)
39	OTHER INFORMATION:	Nucleotide identity unknown
40	NAME/KEY:	allele
41	LOCATION:	(4107)
42	OTHER INFORMATION:	PS9: Polymorphic base A or T
43	NAME/KEY:	allele
44	LOCATION:	(4959)
45	OTHER INFORMATION:	PS10: Polymorphic base A or G
46	NAME/KEY:	allele
47	LOCATION:	(5083)
48	OTHER INFORMATION:	PS11: Polymorphic base G or A
49	NAME/KEY:	unsure
50	LOCATION:	(5459)
51	OTHER INFORMATION:	Nucleotide identity unknown
52	NAME/KEY:	allele
53	LOCATION:	(5506)
54	OTHER INFORMATION:	PS12: Polymorphic base C or A
55	NAME/KEY:	allele
56	LOCATION:	(3558)
57	OTHER INFORMATION:	PS13: Polymorphic base C or T
58	NAME/KEY:	allele
59	LOCATION:	(3804)
60	OTHER INFORMATION:	PS14: Polymorphic base G or A
61	NAME/KEY:	unsure
62	LOCATION:	(6083)
63	OTHER INFORMATION:	Nucleotide identity unknown
64	NAME/KEY:	unsure
65	LOCATION:	(6191)
66	OTHER INFORMATION:	Nucleotide identity unknown
67	NAME/KEY:	unsure
68	LOCATION:	(6242)
69	OTHER INFORMATION:	Nucleotide identity unknown
70	NAME/KEY:	allele
71	LOCATION:	(6707)
72	OTHER INFORMATION:	PS15: Polymorphic base A or G
73	NAME/KEY:	allele

LOCATION: (6420)	
OTHER INFORMATION:	PS16: Polymorphic base C or T
NAME/KEY: allele	
LOCATION: (6475)	
OTHER INFORMATION:	PS17: Polymorphic base G or T
NAME/KEY: allele	
LOCATION: (7045)	
OTHER INFORMATION:	PS18: Polymorphic base G or A
NAME/KEY: allele	
LOCATION: (7396)	
OTHER INFORMATION:	PS19: Polymorphic base G or A
NAME/KEY: allele	
LOCATION: (7515)	
OTHER INFORMATION:	PS20: Polymorphic base G or T
NAME/KEY: unsure	
LOCATION: (8574)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: unsure	
LOCATION: (8581)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: unsure	
LOCATION: (8602)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: unsure	
LOCATION: (8608)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: unsure	
LOCATION: (9878)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: unsure	
LOCATION: (10200)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: unsure	
LOCATION: (10299)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: unsure	
LOCATION: (10555)	
OTHER INFORMATION:	Nucleotide identity unknown
NAME/KEY: allele	
LOCATION: (11085)	
OTHER INFORMATION:	PS21: Polymorphic base C or A
NAME/KEY: allele	
LOCATION: (11174)	
OTHER INFORMATION:	PS22: Polymorphic base C or G
NAME/KEY: allele	
LOCATION: (11252)	
OTHER INFORMATION:	PS23: Polymorphic base C or T
NAME/KEY: allele	
LOCATION: (11389)	
OTHER INFORMATION:	PS24: Polymorphic base C or G

Query Match	48.9%;	Score 739.4;	DB 1;	Length 11942;
Best Local Similarity	85.9%;	Pred. No. 3.8e-173;		
Matches 844;	conservative	1;	Mismatches 132;	Indels 6;
				Gaps 2;

[illegible]







Db 7486 ggaacatgacacagagcgtgagtg 7508

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RESULT 14
US-60-245-225-44/c
; Sequence 44, Application US/60245225
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000883
; CURRENT APPLICATION NUMBER: US/60/245,225
; NUMBER OF SEQ ID NOS: 705
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 12826
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(12826)
; OTHER INFORMATION: n = A,T,C or G
US-60-245-225-44
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Query Match 48.8%; Score 738.2; DB 56; Length 12826;  
Best Local Similarity 85.9%; Pred. No. 7,7e-173;  
Matches 844; Conservative 0; Mismatches 133; Indels 6; Gaps 2;

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Qy 372 CAATGCTGACGCGATGACGAAGTCTCTTATTCATATGCTGTGCTCTCTATGATGG 431
Db 7423 CAGTGTGACGCGATGACGAAGTCTCTTATTCATATGCTGTGCTCTCTATGATGG 7364
Qy 432 CAGCATCTTTGGTACCAACCTGCGCATCTACAGAGTGCATGAAGTGTAGGTGAGCA 491
Db 7363 CAGCATCTTTGGTACCAACCTGCGCATCTACAGAGTGCATGAAGTGTAGGTGAGCA 7304
Qy 492 CTTCCCATTTGACGACGAAGTGTGACCATGATTTGGTCTGATGACGATGACGATGAC 551
Db 7303 CTTCCCATTTGACGACGAAGTGTGACCATGATTTGGTCTGATGACGATGACGATGAC 7244
Qy 552 TGAAGATTGACCTGTGCTCAAAAGTGTGATGAGCCAGTCTGATGATCTCAACCCAGCG 611
Db 7243 AGAGATCGACTTGTGTGAAGAGTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 7184
Qy 612 GGAGTGGACATCATGCGACTGCGAGCGGACGACGAGAGAGAGAGAGAGAGAGAGAGAG 671
Db 7183 TGAAGTGGACATCATGCGACTGCGAGCGGACGACGAGAGAGAGAGAGAGAGAGAGAG 7124
Qy 672 TGTGACATCATCTATGATCTATGATCTGTGCAAAACCACTCTTCTTACACTATCAACT 731
Db 7123 CGGAGCATCATCTATGATCTATGATCTGTGCAAAACCACTCTTCTTACACTATCAACT 7064
Qy 732 CATCATCCCTCGTACTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 791
Db 7063 CATCATCCCTCGTACTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 7004
Qy 792 CTTGCTGCTGAAGATGACACTTGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
Db 7003 CTTGCTGCTGAAGATGACACTTGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6944
Qy 852 GCTCATCTCCAAAGTGTGCTGCCACCTCCCTGATGATACGCTGTGTGTGTGTGTGTGTGT 911
Db 6943 GCTCATCTCCAAAGTGTGCTGCCACCTCCCTGATGATACGCTGTGTGTGTGTGTGTGTGT 6884
Qy 912 CATGTTTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 971
Db 6883 CATGTTTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6824
Qy 972 GCACACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
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Db 6823 GCACACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6764
Qy 1032 GAAGCTGCCACCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
Db 6763 GAAGCTGCCACCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6704
Qy 1092 GCGCTTGAGGAGCGCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
Db 6703 GCGCTTGAGGAGCGCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6644
Qy 1149 TCTGCGGCTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1208
Db 6643 CCGAGGCGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6584
Qy 1209 GCGCTTGAGGAGCGCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
Db 6583 GCGCTTGAGGAGCGCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6524
Qy 1266 CTTGCGGCTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1325
Db 6523 CTTGCGGCTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6464
Qy 1326 GGATGATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1348
Db 6463 GGATGATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6441
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RESULT 15  
US-60-258-250-14/c  
; Sequence 14, Application US/60258250  
; GENERAL INFORMATION:

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; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1001035-PROV
; CURRENT APPLICATION NUMBER: US/60/258,250
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 12826
; TYPE: DNA
; ORGANISM: HUMAN
; NAME/KEY: misc_feature
; LOCATION: (1)...(12826)
; OTHER INFORMATION: n = A,T,C or G
US-60-258-250-14
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Query Match 48.8%; Score 738.2; DB 57; Length 12826;  
Best Local Similarity 85.9%; Pred. No. 7,7e-173;  
Matches 844; Conservative 0; Mismatches 133; Indels 6; Gaps 2;

```
Qy 372 CAATGCTGACGCGATGACGAAGTCTCTTATTCATATGCTGTGCTCTCTATGATGG 431
Db 7423 CAGTGTGACGCGATGACGAAGTCTCTTATTCATATGCTGTGCTCTCTATGATGG 7364
Qy 432 CAGCATCTTTGGTACCAACCTGCGCATCTACAGAGTGCATGAAGTGTAGGTGAGCA 491
Db 7363 CAGCATCTTTGGTACCAACCTGCGCATCTACAGAGTGCATGAAGTGTAGGTGAGCA 7304
Qy 492 CTTCCCATTTGACGACGAAGTGTGACCATGATTTGGTCTGATGACGATGACGATGAC 551
Db 7303 CTTCCCATTTGACGACGAAGTGTGACCATGATTTGGTCTGATGACGATGACGATGAC 7244
Qy 552 TGAAGATTGACCTGTGCTCAAAAGTGTGATGAGCCAGTCTGATGATCTCAACCCAGCG 611
Db 7243 AGAGATCGACTTGTGTGAAGAGTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 7184
Qy 612 GGAGTGGACATCATGCGACTGCGAGCGGACGACGAGAGAGAGAGAGAGAGAGAGAGAG 671
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Db 7183 TGAGTGGGACATCGTGGGCGTGGCGGCGGCGGCAACGAGAACCCGAGACTACGTA 7124  
QY 672 TGTGACATCACCCTATGACTTTCATTCGTCGCAACCAACCTCTTACACTATCACT 731  
Db 7123 CGTGGACATCAGCATGATCATTCATTCATTCGCGCAAGCCGCTCTTCTACCATCACT 7064  
QY 732 CATCATCCCTGCTGCTACATCACTGCTGCGCATCTGCTCTTCTACCTGCCCTAGA 791  
Db 7063 CATCATCCCTGCTGCTACATCACTGCTGCGCATCTGCTCTTCTACCTGCCATCCGA 7004  
QY 792 CTGTGCTGAAGATGACACTTGTATTTCTGTGTGCTAGACATCACTGCTGCTGCT 851  
Db 7003 CTGTGCGGAGAGATGACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6944  
QY 852 GCTCATCTCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911  
Db 6943 GCTCATCTCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6884  
QY 912 CATGTTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971  
Db 6883 CATGTTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6824  
QY 972 GCACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031  
Db 6823 GCACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6764  
QY 1032 GAAGCTGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091  
Db 6763 GAAGCTGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6704  
QY 1092 GCGCTTGAGAGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1148  
Db 6703 GCGCTTGAGAGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6644  
QY 1149 TCTGCGGCTGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208  
Db 6643 CCGAGGCGGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6584  
QY 1209 GCGCTTGCGAGCTGAGCCACTGCA--GCGGCGGCGGCGGCGCTGCTGCTGCT 1265  
Db 6583 GCGCTTGCGGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6524  
QY 1266 CTGTGCGCTCGGAGAGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325  
Db 6523 CTGTGCGCTCGGAGAGGCGGTGGAGCGGCTGCTGCTGCTGCTGCTGCTGCT 6464  
QY 1326 GGATGATGACCAAGTGTGAGG 1348  
Db 6463 GGAGATGACCAAGCGTGAAGT 6441

Search completed: October 16, 2001, 04:32:30  
Job time: 5288 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 03:24:42 ; Search time 5077.39 Seconds  
(without alignments)  
727.378 Million cell updates/sec

Title: US-07-938-154-10

Sequence: 1 ATGCTGGCTTGCATGGCCG.....CAGCTCCAGCTCCAAGTGA 1512

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2711390 seqs, 1221289536 residues

Total number of hits satisfying chosen parameters: 5422780

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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Database : Pending_Patents_NA_NEM:*
1: /cgn2_6/ptodata/1/pna/PCn_NEM.COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEM.COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEM.COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEM.COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEM.COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEM.COMB.seq1:*
7: /cgn2_6/ptodata/1/pna/US09_NEM.COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US06_NEM.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	434.2	28.7	1809	1	PCT-US01-08631-27356	Sequence 27356, A
2	434.2	28.7	3472	6	US-09-898-888-10097	Sequence 10097, A
3	366.8	24.3	1518	5	US-09-948-933-33	Sequence 33, Appl
4	366.8	24.3	1518	5	US-09-948-933-115	Sequence 115, Appl
5	331	21.9	1374	1	PCT-US01-23100-2	Sequence 2, Appl
6	292.4	19.3	1651	1	PCT-US01-08631-7909	Sequence 7909, A
7	287.8	19.0	29194	5	US-09-948-933-451	Sequence 451, Appl
8	287.8	19.0	29194	5	US-09-948-933-533	Sequence 533, Appl
9	250.4	16.6	1554	1	PCT-US01-28206-2	Sequence 2, Appl
10	227	15.0	1482	1	PCT-US01-18835-2	Sequence 2, Appl
11	227	15.0	7132	1	PCT-US01-08631-24011	Sequence 24011, A
12	226.4	15.0	1353	1	PCT-US01-19929-16	Sequence 16, Appl
13	223.6	14.8	601	5	US-09-948-933-1312	Sequence 1312, Appl
14	223.6	14.8	601	5	US-09-948-933-3901	Sequence 3901, Appl
15	177.2	11.7	401	7	US-09-899-995-29	Sequence 29, Appl
16	162.4	10.7	2362	6	US-60-278-258-2883	Sequence 2883, Appl
17	141	9.3	589	6	US-09-823-241-630	Sequence 630, Appl
18	132.2	8.7	2914	5	US-09-950-082-1911	Sequence 1911, Appl
19	132.2	8.7	2914	5	US-09-950-871-130	Sequence 130, Appl
20	124.2	8.2	3728	6	US-09-764-875-2530	Sequence 230, Appl
21	123.2	8.1	2511	1	PCT-US01-08631-15534	Sequence 15534, A
22	117.8	7.8	517	7	US-09-843-620-926	Sequence 926, Appl
23	115.4	7.6	2202	1	PCT-US01-08631-6098	Sequence 6098, Appl
24	106.4	7.0	1642	1	PCT-US01-08631-5095	Sequence 5095, Appl
25	104	6.9	591	1	PCT-US01-08631-7906	Sequence 7906, Appl

## ALIGNMENTS

26	100.6	6.7	24288	1	PCT-US01-23100-1	Sequence 1, Appl
27	100.2	6.6	778	6	US-09-898-8688-6803	Sequence 6803, Ap
28	95.2	6.3	423	7	US-09-747-360-889	Sequence 889, App
29	95.2	6.3	526	8	US-60-253-652-15961	Sequence 15961, A
30	94.6	6.3	440	5	US-09-921-378-17488	Sequence 17488, A
31	90.2	6.0	438	5	US-09-921-378-1824	Sequence 3824, Ap
32	85.6	5.7	443	6	US-09-866-555-2942	Sequence 2942, Ap
33	84.2	5.6	135	1	PCT-US01-08631-6036	Sequence 6096, Ap
34	80.4	5.3	474	6	US-09-904-809-17719	Sequence 17719, A
35	77.2	5.1	211	7	US-09-899-495-115	Sequence 115, App
36	70.8	4.7	349	8	US-60-252-833-3136	Sequence 3136, Ap
37	69.4	4.6	757	6	US-09-758-457-292	Sequence 292, App
38	68.8	4.6	435	7	US-09-764-874-13731	Sequence 13731, A
39	67.4	4.5	515	7	US-09-834-366-11895	Sequence 11895, A
40	66.8	4.4	14033	1	PCT-US01-29206-1	Sequence 1, Appl
41	66.8	4.4	625	6	US-09-898-888-26201	Sequence 26201, A
42	61.8	4.3	444	8	US-60-332-511-141	Sequence 141, App
43	60.2	4.1	12400	1	PCT-US01-19835-51	Sequence 1, Appl
44	60.2	4.0	12400	1	PCT-US01-19835-51	Sequence 1, Appl
45	58.2	3.8	232	7	US-09-824-536-4043	Sequence 4043, Ap

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RESULT 1
PCT-US01-08631-27356
: Sequence 27356, Application PC/TUS0108631
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc
: TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
: FILE REFERENCE: 21272-049
: CURRENT APPLICATION NUMBER: PCT/US01/08631
: CURRENT FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: 09/540,217
: PRIOR FILING DATE: 2000-03-31
: PRIOR APPLICATION NUMBER: 09/649,167
: PRIOR FILING DATE: 2000-08-23
: NUMBER OF SEQ ID NOS: 60736
: SOFTWARE: Custom
: SEQ ID NO 27356
: LENGTH: 1809
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SIMILAR
: LOCATION: (1)..(1806)
: OTHER INFORMATION: 100% homologous to Homo sapiens neuronal acetylcholine
: OTHER INFORMATION: receptor alpha 4 subunit,accession number X85741,Smith-Waterman
: PCT-US01-08631-27356

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28.7%; Score 434.2; DB 1; Length 1809;

[illegible]

Qy	329	TTCCCTTCAAAACACATCTGGCTCCCAAGTGGGTTCTATACAAACATGGTGACGCATGT	388
Db	263	ttcccttcgagctcatcttgcgcgcgaacatcgctcctcaacaaatgcitcagcggagact	3222
Qy	389	ACGAATCTTCCTTCTATTTCCAAATGCTGTGGTCTTCATATATGACAGCATCTTTTGGCTAC	448
Db	323	ttcgggtccccaaccctgcgaaggccaacctgltcatcatcagcgcgggctgcagatgtgactc	3820
Qy	449	CACCTGCCATCTCAACAAGAGTGCATGCACAAGATTAGGTAGTAAGCATCTTCCATTTACACAGC	508
Db	383	ccccggccattctaacaaagctcttcgcagcatcgactgcactctctccctctgcacagc	4422
Qy	509	AGAAATTGCACCATGAAAGTTTGGCTCATGAGCATACACAGCGTACTAGATTACCTGGTGC	568
Db	443	agaaatgcgcacatgtaaattcggctctcccgagctcaagacaaggccaagcttcgcaactcggtga	5022
Qy	569	TCAAAAGTATGTGGCCAGCTGCATATCTTCACACCCAGCGGGAGTGGACATATCG	628
Db	503	acaatgacacgcgcgttgagcacagcttcgtactcttcggagagatgbcagatgggtactcgtgg	5622
Qy	629	CACCTGCCAGCGCCAGACGAACAACGAACCAACGACATCC-----ACATATGTGGACA	679
Db	563	atgcgcgtggcacaactacaacacacagaaagtacgaagtgcgtgcgagttcttaaccggaca	6222
Qy	680	TCACATATACCTTATTCATTTGTGGTGGCAAAACACTCTTCTACACTATCACTCATATCC	739
Db	623	tcaactaagctctgcacatccgcgcgcgtctgcgctctctcaacacataacttaacttaactc	6822
Qy	740	CTGTGGTACTCATACACTTCGTGGCCATCTCGTGGTCTTCTTACCTGCCCTCAGACATGTTG	799
Db	683	ctctgacctgtcatctctccgcctcaacgcgtgtctgtctctcaacctgcctcagatgtgcg	742
Qy	800	AAAGAATGACATTTGTATTTCTGTGGTGTACATCTACAGGTGTTCCTGGTGCATATC	859
Db	743	agaagaatcaagctgtgcactctcgcgtgtctgtctgtcgtatacgtctctcctgtgtcatca	802
Qy	860	CCAAAGTTTGGCTCCCACTCCCTGCATATACCGTGGTGGGCAAGTACTATGTTTA	919
Db	803	cgaagatcaaccgcacacccctcaacttgttaaccacttaacgtgcgaagtaacctgtgttca	8622
Qy	920	CCATGGTGTACTCATCTTCTTCATCTGCACACAGCGTGTGTGCTCATGTGCACACAC	979
Db	863	ceatgtactcttcgtcaacctgtcactcaatgtaacagctctcgtgtcgtcaacgtgcacacac	922
Qy	980	GCTACGCTACACACGACACACATGCGCCCTCGGGTCAAGGTGGTTCTTCTGTGGAAGATGC	103
Db	923	gtctgcacagcaagcaacacatgtcccaacctgcggtaagcaaggtctctcctgtgacatcgtgc	982
Qy	1040	CCACCTGTCTTCTCTGACGAGGC 1064	
Db	983	caagctgtctctcatagaaagagcc 1007	

; LOCATION: (1)...(3472)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-898-888-10097

Query Match	28.7%;	Score 434.2;	DB 6;	Length 3472;
Best Local Similarity	66.7%;	Pred. No. 3.3e-94;		
Matches 657; Conservative	0;	Mismatches 313;	Indels 15;	Gaps 2;

[illegible]







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Db      1002  gattttatcgaacatacccaatatcatgt 1034

RESULT      6
PCT-US01-08631-7909
; Sequence 7909, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/TUS01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 7909
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1455)..(1520)
; OTHER INFORMATION: 77% homologous to Homo sapiens acetylcholine receptor beta-
; OTHER INFORMATION: subunit preproteins, accession number X14830, Smith-Waterman Score-
; OTHER INFORMATION: 101.
; CCT-US01-08631-7909

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[illegible]

Db 598 aatcaacattcatatgaaggacttctcatcttgagaatctgccaagtggaggaatcatcaacagcc 657  
QY 636 AGGCGACAGCAGCAGAGAACCCAGACAGCTCCACCTATGT-----GGA 677  
Db 658 cctctggcctcaatcccaagcctccaaagatctcttaagaggaaggaaggaacagcgccacgga 717  
QY 678 CATACACCTATGACTTCATCATATTCGTGCGAAACCACTCTTCTACTATATCAACTCATCATAT 737  
Db 718 agtcatctctcatctcatcatcaatccagcgaagcctctctctcatcctctgcaacagctcatgc 777  
QY 738 CCCCCTGAGCTATCATACCTCGCTGAGCCATCTGAGTCTTACTGCCCCCTCAACTGTGG 797  
Db 778 ccgatctcatctcatctactactctctctggccatctctgcctctctcatcctgcaacacagatcag 837  
QY 798 TGAAGAAGATGACACTTGTATTTCTGTGCTGAGCTAGAGCAACACAGGATGTCTTCAGTGCAT 857  
Db 838 agagaagaatggagcctccatcaactctctggccctcgagcccttactgtgtcttcgctgcgtc 897  
QY 858 CTCCAGAGATTGTGGCCCTCCGACCTCCCTCTCGATGTATGATGAGCGTGGGAGAGTACCTCATGTT 917  
Db 898 ggtctgacaaagatgacctgagacctcatcatcatcagatcatatcatcaagttaacctcatgct 957  
QY 918 TACCATGTGATGATGACCTTCTTCATCTGCATGTCACACAGCGATGTGATGACATGTAGACCA 977  
Db 958 taacataagttccctgcgtacacactcttcagatcacttctgttgcgtgtcttctcaacccagca 1017  
QY 978 CGCGTGGCCTTACCAACCACTACGAGCCGCCCCGAGTGCATGATGATGATGATGATGATGATGAT 1037  
Db 1018 cgtgtaccccaacacacacacacaaagccctcttggtgcgttcagatctcatctcatcaaac 1077  
QY 1038 GCCGACCTTGTCTTCTCTGTCAGACGCCACCGCTGTGTCACGTCAAGCTCTGCGCTT 1097  
Db 1078 tccgtgttactcgtgtctcaaaaagcccaaaccccgagagagacactgtagtccgagccccc 1137  
QY 1098 GAGAGAGCCGCAACGACGAGACGTGA--GAGCGAGAGCGGATTTCTTCCGTGAAGTCTGGCG 1155  
Db 1138 tcaactcttctctccagagaagtgtgtggttcggtggaagaagatgataatcttaccgcgaa 1197  
QY 1156 GCAGACCATGTACCTGCTTTGTCTCAACCCCTGTCATCATGATGACAGAGGCTTGGCGGAGCTTTC 1215  
Db 1198 ggcgcgaagtgtatctctctctcccaaaccaatagattccagactgtatgtctgcgcc 1257  
QY 1216 CGAGGTAGAGCCCATGTCAGACGCGCGCGGCGGCTGTGTGTGGGACCATGACGTGAGGCTTC 1275  
Db 1258 tgaatcgcgcgcatattatcatgtatgttccaaacgcggcgtgtgcccgtcttcggag--cta 1315  
QY 1276 CGGGAAGACAGTGTGATGAGCGGTAGCGTCACTTATGTCGAGACACATGCGAAGATGATGATGATGAC 1335  
Db 1316 cggagagatgctctctctcatcatcatcatcatcgtctcgcagcagctgcaggaacgcgaggaaccac 1375  
QY 1336 CAGAGTGTAGAGGAGAGACTGTGGAATACGTTCGCCATGTGATGACAGCGGCTGTCGCTG 1395  
Db 1376 gtagcgcctgaagaagagacgcgagcttgtaggcagctgtagtgagacgcctctctctgtgg 1435  
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RESULT 7  
US-09-948-933-451  
; Sequence 451, Application US/09948933  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: C1000787  
; CURRENT APPLICATION NUMBER: US/09/948,933  
; PRIOR APPLICATION NUMBER: 2001-09-10  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 6404

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 451
; LENGTH: 29194
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(29194)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-933-451
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Query Match          19.0%: Score 287.8; DB 5; Length 29194;
Best Local Similarity 64.3%: Pred. No. 7.2e-59;
Matches 452; Conservative 0; Mismatches 242; Indels 9; Gaps 1:

QY 372 CAATGCTGACGGCATGTACGAGTCTCTTCTTCAATTCATGCTGTGCTCTCTATGATGG 431
Db 20418 cagtgctgttgaggatltccaggtgagcagaagcaccacttaactcaagtacactgg 20477
QY 432 CAGCATCTTTGGCTACACCTGCTCCATCTACAAAGTGATGCAAGATTGAGTGAAGCA 491
Db 20478 ggaagtgacttgatctccgcgcacatcttaagagctccctgtaaaatcgagctgacct 20537
QY 492 CTTCCTATTTGACCAAGATGACCAATGAAATTTGCTCATGAGACTGACACCGTAC 551
Db 20538 ctcccgcttgatattacaaaacgtacatgaagttcggttcgttcctacgataaggg 20597
QY 552 TGAGATTGACCTGGTGGCTCAAAAGTATGATGGCCAGTGTGATGCTTGCATACACCGG 611
Db 20598 gaaatcgatctgtctctgtctgtctctctcctacatgaactcaagacatacttgagagcg 20657
QY 612 GGAGTGGGACATCATCCGACTGCGCAGCGAGCAAGCAAGAACCCAGACACTGCG----- 666
Db 20658 cgagtgagccatctcaaaagcccaagccatacaagacgacatcaagtaactctgtcgga 20717
QY 667 ----ACCTATGTGACATCATCACTTATGATCTTGTGCTGCAACCACTCTTTTACAC 722
Db 20718 ggaagatctaacccgcacatacatctcgctgacatccgcgcgcctgtccctgtctctaac 20777
QY 723 TATCAACTCATCATCCCTGCGTACTCATCACTGCGTGGCCATCTGCTTCTTACCT 782
Db 20778 catcaactctatctatctccctgtctctctctctcctcctgtctgtctctctctaac 20837
QY 783 GCCCTCAGACTGTGTGTAAGATGACACTTGTATTTCTGTGCTGTAGCACTCAAGGT 842
Db 20838 gccctcgcagccggtggaagagtgacccctgtcatctctctctcctcctcctcgcgtg 20897
QY 843 GTTCCTGCTGCTCATCTCCCAAGATGTCGCCACCTGCCACGTCCGATGACGGTGTGGG 902
Db 20898 gttctcctgtgtatctatctgacatccctcctccactcgtgtcatccctcctgtatgg 20957
QY 903 CAAGTACCTCATGTTTACCATGGGTGATGACCTTCTCCATGCGACACCGGTGTGT 962
Db 20958 agagtaacctctgttcaacatgatttttgaacctgtccatctgcaacccgctcgtcgt 21017
QY 963 GGTCAATGTGACACCGCTGCTTACCAAGATGTCGCCACCTGCGTGGGTGCAAGGTGT 1022
Db 21018 gctcaacgtgacacagaaaccccgagacacacaaatgagtgagtgagactgt 21077
QY 1023 CTTCCTGGAAGAGTCCACCTGCTTCTTCTGCAAGCAAGCA 1065
Db 21078 attcttgaacctgtcccccagtgatctgtcatgacagcgca 21120

RESULT
US-09-948-933-533
; Sequence 533, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
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; FILE REFERENCE: CLO00787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 533
; LENGTH: 29194
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(29194)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-933-533
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Query Match          19.0%: Score 287.8; DB 5; Length 29194;
Best Local Similarity 64.3%: Pred. No. 7.2e-59;
Matches 452; Conservative 0; Mismatches 242; Indels 9; Gaps 1:

QY 372 CAATGCTGACGGCATGTACGAGTCTCTTCTTCAATTCATGCTGTGCTCTCTATGATGG 431
Db 20418 cagtgctgttgaggatltccaggtgagcagaagcaccacttaactcaagtacactgg 20477
QY 432 CAGCATCTTTGGCTACACCTGCTCCATCTACAAAGTGATGCAAGATTGAGTGAAGCA 491
Db 20478 ggaagtgacttgatctccgcgcacatcttaagagctccctgtaaaatcgagctgacct 20537
QY 492 CTTCCTATTTGACCAAGATGACCAATGAAATTTGCTCATGAGACTGACACCGTAC 551
Db 20538 ctcccgcttgatattacaaaacgtacatgaagttcggttcgttcctacgataaggg 20597
QY 552 TGAGATTGACCTGGTGGCTCAAAAGTATGATGGCCAGTGTGATGCTTGCATACACCGG 611
Db 20598 gaaatcgatctgtctctgtctgtctctctcctacatgaactcaagacatacttgagagcg 20657
QY 612 GGAGTGGGACATCATCCGACTGCGCAGCGAGCAAGCAAGAACCCAGACACTGCG----- 666
Db 20658 cgagtgagccatctcaaaagcccaagccatacaagacgacatcaagtaactctgtcgga 20717
QY 667 ----ACCTATGTGACATCATCACTTATGATCTTGTGCTGCAACCACTCTTTTACAC 722
Db 20718 ggaagatctaacccgcacatacatctcgctgacatccgcgcgcctgtccctgtctctaac 20777
QY 723 TATCAACTCATCATCCCTGCGTACTCATCACTGCGTGGCCATCTGCTTCTTACCT 782
Db 20778 catcaactctatctatctccctgtctctctctcctcctcctgtctgtctctctctaac 20837
QY 783 GCCCTCAGACTGTGTGTAAGATGACACTTGTATTTCTGTGCTGTAGCACTCAAGGT 842
Db 20838 gccctcgcagccggtggaagagtgacccctgtcatctctctcctcctcctcgcgtg 20897
QY 843 GTTCCTGCTGCTCATCTCCCAAGATGTCGCCACCTGCCACGTCCGATGACGGTGTGGG 902
Db 20898 gttctcctgtgtatctatctgacatccctcctccactcgtgtcatccctcctgtatgg 20957
QY 903 CAAGTACCTCATGTTTACCATGGGTGATGACCTTCTCCATGCGACACCGGTGTGT 962
Db 20958 agagtaacctctgttcaacatgatttttgaacctgtccatctgcaacccgctcgtcgt 21017
QY 963 GGTCAATGTGACACCGCTGCTTACCAAGATGTCGCCACCTGCGTGGGTGCAAGGTGT 1022
Db 21018 gctcaacgtgacacagaaaccccgagacacacaaatgagtgagtgagactgt 21077
QY 1023 CTTCCTGGAAGAGTCCACCTGCTTCTTCTGCAAGCAAGCA 1065
Db 21078 attcttgaacctgtcccccagtgatctgtcatgacagcgca 21120

RESULT
US-09-948-933-533
; Sequence 533, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
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Db 6274 AGACCGCTTCTGTTCCCTATTGCGCAGAAATCCAGAGATTCTCTAGAGCTGCGG 6215
Oy 896 TGTGGGCAAGTACCTCATTTTACCATGTGTGCTAGTACCTTCTCCATGTCACAGCG 955
Db 6214 TCCGGGCGAGGTCCTTATTTTTCGTATGTTGTCGACAGCTCATGTATGTAATTTGCG 6155
Oy 956 TGTGTGTCTCAATGTCAGCAGCGCTGCTACAGCGACACATGAGCCCTCGGTGTC 1015
Db 6154 TCATCGTGCTCAACGTCCTCCAGGAGCGCCACACACCGCATGTCCCGGCGTGC 6095
Oy 1016 AGGTGCTCTCTGAGAGCTGCCACCTGCTCTTCTGACAGCAGCCCA 1070
Db 6094 GCCACGTTCTCGAGACTGCTCCGCGCTCCTCGGCGTCCCGCGCGCCCGCA 6040

RESULT 12
PCT-US01-19929-16
; Sequence 16; Application PC/TUS0119929
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LTD.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029
; CURRENT APPLICATION NUMBER: PCT/US01/19929
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US01-19929-16

Query Match 15.08; Score 226.4; DB 1; Length 1353;
Best Local Similarity 54.7%; Pred. No. 1.7e-44;
Matches 499; Conservative 0; Mismatches 401; Indels 12; Gaps 2;

Oy 176 TGACTGACAGCTCATGTATCATTTGCTGCTCATTTAGTGTGACAGCGAGAGAGA 235
Db 164 tgaatggaacctggaagtgaactgtccagatcagcatcagatgagatgagacagag 223
Oy 236 TCATGACACCAATGTCTGCTGACGAGAGTGGAGATTACCGCTTCACATGCAAGC 295
Db 224 tgcctgacctgctatctgtgatacagagagagagacagatgctctactcagatgagac 283
Oy 296 CTGAGGACTTGACATATGTAAGAAAGTCCGGCTCCCTTCAAAACATCATGTGGCTCCAG 355
Db 284 ccaatgctcatggtgagcctgagatgcatcgcacccacagatctgtgtgagcag 343
Oy 356 ATGTGCTTCATACACATGCTGACGCGCATGTACGAAGTCTCTTCTATTCGAATGCTG 415
Db 344 acatcgtactctataaagaagcagcagcagcctccaggttccgacagcaacagctg 403
Oy 416 TGTCTCTCTATGATGAGAGATCTTTTGGTACCACTGCACTGCAATACAGAGTGCATGA 475
Db 404 tctcgcccaagatgagcgccgtgctggaagcgccgagccatcaagcagcgtcgcc 463
Oy 476 AGATTGAGGTGACACCTTCCCATTTTGACGAGAAATTCACACCATGAAGTTTCGCTCAT 535
Db 464 gctgtagatgtagcagccttccgttcgacgcagcagcactgagcctgagctcgccct 523
Oy 536 GGACTCTGACGAGTATGAGATGTGCTGCTCAAAAGTGTGGCAGTGTGATG 595
Db 524 ggaactcaagggagacacaaactgagtgctgagcgcgcgagcagcagcagcagcagc 583
Oy 596 ACTTCACACCCAGCGGAGAGTGGAGATCATGCATGCGACGAGGCCAGCAGAGAAACC 655
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Db 584 acttcgtgagagacgtgtagtgagcgctgctgagcatgcccgcgagcgagcgctgctca 643
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Db 644 cctacgctgctgctcgcagacccatcccgagcatcctcagctgctgctgctgctgctg 703
Oy 707 AACCACTTCTTACACTATACACTATCATCATCCCTGGCTACTTCACTACCTGCGAGCA 766
Db 704 ggcgcgcgcctcagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 763
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Db 824 tgcctgctcctacacgtcctcctcctgctgctgctgctgctgctgctgctgctgctg 882
Oy 887 ATGTACGCTGTGTGGCAAGTACCTCATGTTTACCAAGTGTGCTACTCATCTTCATCG 946
Db 883 --gtgcgctcctcagagagactacatgcccacatgacatgctacatctcacaag 940
Oy 947 TCACGAGCGTGTGTGCTCATGTGACACCGCTCCGCTTCCACAGCAGACCATGAGGCC 1006
Db 941 cactccacatcctatcagatgacatcgtcactgctgctgctgctgctgctgctgctg 1000
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RESULT 13
US-09-948-933-1312/C
; Sequence 1312; Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO00787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1312
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-948-933-1312

Query Match 14.8%; Score 223.6; DB 5; Length 601;
Best Local Similarity 63.5%; Pred. No. 6.4e-44;
Matches 362; Conservative 0; Mismatches 199; Indels 9; Gaps 1;

Oy 372 CAATGCTGACGCGCATGTACGAAGTCTCTTCTTATTCATGCTGTGCTGCTCTATGATG 431
Db 571 CAATGCTGTGGGATTTCCAGTGGACAGCAAGACAAAGCTTACATCAAGTACACTGG 512
Oy 432 CAGACATCTTTGGCTCCACCTGCTCATACAGAGTGCATCAAGATTTGAGTGAAGCA 491
Db 511 GAGGAGACTTGATGATCCGCGCATCTTTAAGAGCTCTCTTAAGATGAGTACCTGA 452
Oy 492 CTTCCTCATTTGACACAGATTTGACACATGAGATTTCCTCTATGACTACGACCGTAC 551
Db 451 CTTCCTCATTTGATTTACAAAGCTGTACATGAAGTTCTGCTGCTCATGATTAAGC 392
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OM of: US-07-938-154-10 to: p1r\_68:\* out\_format : pfs  
Date: Oct 16, 2001 6:02 AM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

## Command line parameters:

-MODEL=frame+np,model -DEV=xlp  
-O=/cgn2.1/uspro.spool/5981193/rnat.15102001.132923.21328/app-query.fasta.1.1596  
-DB=p1r\_68 -PMT=fastan -SUFFIX=pr -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500  
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DEEXT=7.000 -START=1 -MATRIX=blastm62 -TRANS=human40.cdi  
-LIST=45 -DOCALL=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
-MAXLEN=2000000000 -USER=5981193.@cgn1.1.83 -NCPU=6 -ICPU=3  
-LONGLOG -NO\_XLPXY -WAIT -THREADS=1

## Search information block:

Query: US-07-938-154-10  
Query length: 1512  
Database: p1r\_68\*  
Database sequences: 219241  
Database length: 76174552  
Search time (sec): 70.720000

Sequence	Strd Orig	%score	Escore	len	Documentation
p1r2:JH0174	+ 2666.00 3710.86	2.2e-199	503	1	nicotinic acetylcholine recept
p1r2:SI0505	+ 2432.00 3363.80	3.4e-181	502	1	nicotinic acetylcholine recept
p1r1:ACCHN	+ 2129.00 2960.86	1.3e-157	491	1	nicotinic acetylcholine recept
p1r2:A33218	+ 1743.00 2422.20	1.3e-127	479	1	nicotinic acetylcholine recept
p1r2:SI1703	+ 1660.50 2307.19	3.5e-121	459	1	nicotinic acetylcholine recept
p1r2:G04221	+ 1630.00 2263.92	8.3e-119	498	1	nicotinic acetylcholine recept
p1r2:B33721	+ 1581.00 2195.52	5.4e-115	495	1	nicotinic acetylcholine recept
p1r2:A30992	+ 1567.00 2175.60	6.6e-114	517	1	probable nicotinic acetylcholin
p1r1:ACCH2N	+ 1224.00 1696.43	3.2e-87	528	1	nicotinic acetylcholine recept
p1r2:A26436	+ 1210.50 1676.13	3.6e-86	625	1	nicotinic acetylcholine recept
p1r2:JCH4021	+ 1204.50 1667.72	1.1e-85	627	1	nicotinic acetylcholine recept
p1r1:ACCH4N	+ 1201.00 1662.90	1.0e-85	622	1	nicotinic acetylcholine recept
p1r2:A24572	+ 1198.50 1661.30	3.0e-85	499	1	nicotinic acetylcholine recept
p1r2:B37014	+ 1197.50 1659.69	3.6e-85	512	1	nicotinic acetylcholine recept
p1r2:SI60589	+ 1197.00 1656.28	4.0e-85	495	1	acetylcholine receptor alpha ch
p1r2:A40110	+ 1195.00 1656.21	5.7e-85	511	1	nicotinic acetylcholine recept
p1r2:A53956	+ 1179.50 1634.70	9.1e-84	503	1	nicotinic acetylcholine recept
p1r2:A37040	+ 1173.00 1635.64	2.9e-83	502	1	nicotinic acetylcholine recept
p1r2:T03289	+ 1148.50 1591.57	2.4e-81	494	1	nicotinic acetylcholine recept
p1r1:ACFFA1	+ 1127.00 1560.36	1.1e-79	567	1	nicotinic acetylcholine recept
p1r2:SI1899	+ 1074.00 1487.42	1.5e-75	500	1	nicotinic acetylcholine recept
p1r2:SI0548	+ 1060.50 1469.27	1.6e-74	461	1	acetylcholine receptor alpha-su
p1r1:ACRYA1	+ 1057.50 1465.08	2.8e-74	461	1	nicotinic acetylcholine recept
p1r2:SI2359	+ 1054.00 1458.57	5.3e-74	557	1	nicotinic acetylcholine recept
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p1r1:ACCPA2	+ 1032.50 1428.26	2.5e-72	576	1	nicotinic acetylcholine recept
p1r2:SI6333	+ 1019.00 1411.22	2.8e-71	466	1	nicotinic acetylcholine recept
p1r2:SI6383	+ 1016.50 1407.90	4.3e-71	457	1	nicotinic acetylcholine recept
p1r2:A24383	+ 1014.50 1405.11	6.2e-71	457	1	nicotinic acetylcholine recept
p1r1:ACBOA1	+ 1014.50 1405.11	6.2e-71	457	1	nicotinic acetylcholine recept
p1r2:B39218	+ 1014.00 1404.46	6.8e-71	454	1	nicotinic acetylcholine recept
p1r2:AS5972	+ 1011.50 1400.95	1.1e-70	455	1	nicotinic acetylcholine recept
p1r2:AS3523	+ 1009.00 1397.03	1.7e-70	464	1	nicotinic acetylcholine recept
p1r1:ACCHUA1	+ 1008.00 1396.93	2.0e-70	457	1	nicotinic acetylcholine recept
p1r2:SI49458	+ 1004.50 1381.37	3.7e-70	445	1	acetylcholine receptor alpha-su
p1r1:ACRYB1	+ 1003.00 1381.40	4.9e-70	493	1	nicotinic acetylcholine recept
p1r2:A25336	+ 1003.00 1388.26	4.9e-70	501	1	nicotinic acetylcholine recept
p1r2:SI5116	+ 998.50 1382.80	1.1e-69	453	1	nicotinic acetylcholine recept
p1r1:ACFFNN	+ 996.50 1378.15	1.7e-69	521	1	nicotinic acetylcholine recept
p1r2:A28529	+ 995.00 1377.87	2.0e-69	457	1	nicotinic acetylcholine recept
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p1r1:ACCHD1 + 993.50 1374.79 2.7e-69 513 1 nicotinic acetylcholine rece  
p1r2:SI06893 + 991.50 1372.89 3.8e-69 462 1 nicotinic acetylcholine rece  
p1r1:ACCHAN + 991.00 1372.31 4.2e-69 456 1 nicotinic acetylcholine rece  
p1r2:A35721 + 987.00 1366.80 8.5e-69 452 1 nicotinic acetylcholine rece

seq\_name: p1r2:JH0174

## seq\_documentation\_block:

nicotinic acetylcholine receptor beta-2 chain precursor - rat  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 29-Jan-1999  
C.Accession: JH0174; A61638; S06435  
R.Denieris, E.S.; Connolly, J.; Boulter, J.; Wada, E.; Wada, K.; Swanson, L.W.; Patric  
Neuron 1, 45-54, 1988  
A.Title: Primary structure and expression of beta 2; a novel subunit of neuronal nico  
A.Reference number: JH0174; MUID:90166479  
A.Accession: JH0174  
A.Molecule type: mRNA  
A.Residues: 1-503 <DEN>  
A.Cross-references: GB:L31622; NID:g468921; PID:g468922  
A.Experimental source: brain  
R.Schoepfer, R.; Whiting, P.; Esch, F.; Blacher, R.; Shimasaki, S.; Lindstrom, J.  
Neuron 1, 241-248, 1988  
A.Title: cDNA clones coding for the structural subunit of a chicken brain nicotinic a  
A.Reference number: JH0175; MUID:90166513  
A.Accession: A61638  
A.Molecule type: protein  
A.Residues: 29-33, 'X', 35-37, 'X', 39, 'X', 41, 'X' <SCH>  
A.Experimental source: brain  
A.Superfamily: acetylcholine receptor  
C.Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein  
F.1-29/Domain: signal sequence #status predicted <Sig>  
F.29-303/Product: nicotinic acetylcholine receptor beta-2 chain #status predicted <MA  
F.237-263/Domain: transmembrane #status predicted <TM>  
F.270-291/Domain: transmembrane #status predicted <TM>  
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F.514,171,486/Binding site: carbohydrate (Asn) #status predicted

## alignment\_scores:

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Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-07-938-154-10 x JH0174 ..  
Align seg 1/1 to: JH0174 from: 1 to: 503

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51 CAGCTTCTTGTGCTGTGCTCAGGCGTTTGGCACTGACAGAGAGAC 100
|||||
17 eserLeuLeuTrpLeuCysSerGlyValLeuGlyThrAspThrGluGua 34
101 GCGTAGGAGCATCTTATGATCCCTCCGCTATACAGCGATTGCT 150
|||||
34 rglLeuValGlnHisLeuLeuAspProSerArgTrpGlyAsnHisLeuIleArg 50
151 CAGACTTACTAAGGCTCTGAGCTGTGACTGTACAGCTCATGATCAT 200
|||||
51 ProAlaThrAsnGlySerGluLeuValThrValGlnLeuMetValSerIe 67
201 GCGCTGACCTATTAGTGTGACGAGCGGAGCAGATCATGACCAACG 250
|||||
67 uAlaGlnLeuIleSerValHisGlnArgGluGlnIleMetThrAsnVal 84
251 TCTGCTGACCCAGAGAGTGGAGAGATTACCGCTGCACATGAGAGCTG 300
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84 alTrpLeuThrGlnGlnIleTrpGluAspTyrArgLeuThrTrpIysProGlu 100
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101 ASPPhaspasmethylsulvalalyleuProserLysHisIleTyrPle 117
351 CCCAGATGTGTTCTATACAAATGCTGACGGCATGTACGAAGTCTCT 400
117 uProaspvalalyleuTyrasnAsnalaspGlyMethylcyluValSerP 134
401 TCTATTCATGCTGTGCTCTCTATGATGAGCATCTTTGGGTACCA 450
134 heTyrserasnAlavalalserTyrAspGlySerIlePheTyrleuPro 150
451 CCTGCCATCTACAAAGTGTCAAGATGTGAGTGAAGCACTTCCATT 500
151 ProlalileTyrLysSerAlacysLysIleGluValLysHisPheProh 167
501 TGACGACGAAATTCACCATGATGAATTCGCTCATGACCTACGACGTA 550
167 eaSPGInGlnAsnCySthMetLysPheArgSerTyrPheTyrAspArgT 184
551 CTGAGATTGACCTGGTGTCAAAAGTATGATGGCCAGTCTGGATGACTTC 600
184 hrcIuIleaspleuValIleuLysSerAspValAlaSerLeuAspAsphe 200
601 ACACCCAGGGGAGTGGGACATCATCGACCTGCCAGGCCGACGCAACGA 650
201 ThrProserGlycIuTyrPaspIleleAlaLeuProGlyIhArgAsnG1 217
651 GAACCCAGACGACTCCACTATGTGACATCACCATTGACTTCATCATTC 700
217 uasnProaspSerThrTyrValAspIleThrTyrAspPheIleleAla 234
701 GTGCAACACCATCTCTACATCAACCATCATCATCCCTGGGTATCTC 750
234 rgrArgLysProleuPheTyrThrIleasnleuIleIleProCysValleu 250
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251 IleThrSerleuAlaIleleuValPheTyrleuProSerAspCysGlyG1 267
801 AAAGATGACACTTTGATTTCTGTGCTGTACACTCAGCGGTGTTCTGTC 850
267 uLysMetThrleuCySleSerValleuValleuThrValPheLeuL 284
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284 euLeuIleSerLysIleValProProThnSerLeuAspValProleuVal 300
901 GGCAGATCCTCATGTTTACATGCTGTAGTCCATCTCTCCATGCTCAC 950
301 G1LysIleTyrleuMetPheThrMetValleuValIthrPheSerIleValIth 317
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317 rSerValCySvalleuAsnValHisHisArgSerProThrThrHisStrm 334
1001 TGGCCCCCTGGGTCAAGTGTGCTCTCTGGAAGAAGTGGCCACCTGCTC 1050
334 eLalProTyrPallLysValIalPheleGluLysleuProThrleuLeu 350
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351 PheleGluGlnleProArgHisArgCySalaArgIlnArgLeuArgLeuAr 367
1101 GAGGGCGCGAGGAGCGTGGAGGGGAGCGGTTTCTTCGTTGGAAGTTC 1150
367 gAlArgIlnArgIlnArgIlnArgIlnArgIlnArgIlnArgIlnArgI 384
1151 CTGCGGCTGACCCATGTACTCTGTTGTCAACCTGTGATCAGTGCAGGCG 1200
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401 LeuAlaGlyAlaPheArgAlaGluProThrAlaAlaGlyProGlyArgSe 417
1251 TGTGGGCGCATGACACTGTGGCTTCGCGGAAGACAGTGGATGGCTACGCT 1300
417 rValGlyProcysSerCySglyLeuArgGluAlaValAlaSpGlyValArgP 434
1301 TCATGGCGGACCATGAGGAGTGAAGTATGATGACACGAGTGTGAGGGAG 1350
434 heIlaAlaAspHisMetLysGserGlnAspAspArgIlnSerValArgGlu 450
1351 GACGTGAATACGTTGCCATGATGACACCGCTGTTCCGTGGAGATCTT 1400
451 AspTyrLysTyrValAlaMetValIleAspArgleuPheleuTyrPlePh 467
1401 TGTCTTTGTGTGTCTTGTGGACGTTGGCATGTCTCTGACCTCTCT 1450
467 eValPheValCySvalPheGlyThrValGlyMetPheleuGlnProleuP 484
1451 TCCAGACTACACCTGCGACTCTCTCCACCGCTGACACTGACGCTCC 1500
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501 SerSerLys 503

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nicotinic acetylcholine receptor beta-2 chain precursor - human
C:Species: Homo sapiens (man)
C:date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
C:Accession: S10505
R:Amnd: R.; Lindstrom, J.
Nucleic Acids Res. 18, 4272, 1990
A:Title: Nucleotide sequence of the human nicotinic acetylcholine receptor beta-2 sub
A:Reference number: S10505; M0ID:90332444
A:Accession: S10505
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <ANA>
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C:Keywords: neurotransmitter receptor; transmembrane protein

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US-07-938-154-10 x S10505 ..
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11 LeuLeuGlyPheGlyLeuLeuArgLeuCySserGlyValAlaIlePrlpLysTras 27
90 CACAGAGAGCGGCTAGTGGAGCATCTCTTATGATCCCTCCCGGTATACAA 139
27 pThrGluGluArgleuValAlaGluHisleuLeuAspProSerArgTyrAsnL 44
140 AGCTGATGCTGCGACCTACTAAGCGCTCTGAGCGGTGAGTACAGAGCT 189
44 ySerleuIleArgProAlaThrAsnGlySerGluLeuValIlnValGlnleu 60
190 ATGATATCATTTGGCTCAAGCTATTAGTGTGCAGAGCGGAGAGCATATCAT 239
61 MetValSerleuAlaGlnleuIleSerValHisGluArgGlnGlnIleMe 77

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240 GACACCAATGTCGTGAGTACCAGGAGTGGAGATTACCGCTCAT 289
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290 GGAAGCTGAGACTTGGACATATGAAAGAGTCCGGCTCCCTTCAAA 339
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94 rplyrproglnglupheaprasnmetylsvalargleuproseryls 110
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340 CACATCTGCTCCAGATGTGTTCTATACAACAATGCTAGCGCATGA 389
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127 tglvalserphetyserasnalaivalsertrynspolyserlier 144
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277 rValrheuleuulleserYalileuValProthrSerleuAspY 294
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1137 CTTCGCTGAGAGTCTCGCGGCTGACCCCATGATACCTGCTTGTCAACCTG 1186
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1187 CARGAGTGCAGGCTGGCTGGGCTTTCCGAGCTGAGCCCACT...GCA 1233
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394 laSerValglnnglYleuAlaaglylaPheglYalagluProalarProal 410
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1234 GCGGAGCCCGGCGGCTCTGTGGGCGCATGCGAGCTGTGCTGCGGAGAGC 1283
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1334 ACCAGACTGTGACGAGAGACACGAGAAATACGTGGCATGGTATGACAGCC 1383
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444 spglaserValsergluAsptryprlystYalAlaMetvalAlleasprarg 460
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1384 CTGTGCTGTGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1433
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461 leupheultrprleuphevalrphelalCysValrphelYthrileglYme 477
|||||
1434 GTTCCTGACGCTCTCTTCAGAACTACATGCGCATGCTTCTCTGCGACC 1483
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nicotinic acetylcholine receptor nonalpha chain precursor, neuronal - chicken
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C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C:Accession: S00380; A38757; JH0175; PS0297
R:Net, P.; Oneyser, C.; Alliod, C.; Countier, S.; Ballivet, M.
EMBO J. 7, 595-601, 1988
A:Title: Genes expressed in the brain define three distinct neuronal nicotinic acetyl
A:Reference number: S00376; M01D:88283624
A:Accession: S00380
A:Molecule type: DNA
A:Residues: 1-491 <NER>
A:Cross-references: GB:X07353; GB:Y00834; NID:962945; PIDN:CA30286.1; PID:9871038
A:Accession: A38757
A:Molecule type: mRNA
A:Residues: 1-491 <NER2>
A:Cross-references: EMBL:X07353; NID:962945; PIDN:CA30286.1; PID:9871038
R:Schoepfer, R.; Whiting, P.; Esch, F.; Blacher, R.; Shimaseki, S.; Lindstrom, J.
Neuron 1, 241-248, 1988
A:Title: cDNA clones coding for the structural subunit of a chicken brain nicotinic a
A:Reference number: JH0175; M01D:90166513
A:Accession: JH0175
A:Molecule type: mRNA
A:Residues: 1-491 <SCH>
A:Cross-references: GB:X53092; GB:X53566; NID:962957; PIDN:CA37258.1; PID:962958
A:Accession: PS0297
A:Molecule type: protein
A:Residues: 19-58 <SC2>
C:Genetics:
A:Introns: 15/1; 63/3; 115/2; 435/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-491/Product: nicotinic acetylcholine receptor nonalpha chain #status experimenta
F:228-251/Domain: transmembrane #status predicted <TM1>
F:259-277/Domain: transmembrane #status predicted <TM2>
F:293-314/Domain: transmembrane #status predicted <TM3>
F:450-468/Domain: transmembrane #status predicted <TM4>
F:44,161/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

F:148-162/Disulfide bonds: #status predicted

## alignment\_scores:

Quality: 2129.00 Length: 480  
 Ratio: 4.700 Gaps: 6  
 Percent similarity: 94.375 Percent identity: 85.208

## alignment\_block:

US-07-938-154-10 x ACCHNN

Align seg 1/1 to: ACCHNN From: 1 to: 491

```

79 TTGGGAAGTGCACAGAGAGCGGCTAGTGGAGCATCTTCTAGATCCGCT 128
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 LeucylthraspthrghlgluargleuValglutylleuLeuAspProth 33
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
129 CCGCTTAACAGCTGATGTCGCTCCAGCTACTAAGCGCTCTAGTGGTGA 178
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
33 ArgTyrAsnLysLeuIleArgProAlaThrAsnGlySerGlnLeuValT 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
179 CTGTACAGCTATGATGATCATGTCGCTCAGCTCATAGTGTGACAGCG 228
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50 hrValGlnLeuMetValSerLeuAlaGlnLeuIleSerValHisGluArg 66
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
229 GACCATCATGACACCAATGCTGCTGACCGCAGCAGAGTGGGAAGATT 278
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 GluGlnIleMetThrThrAsnValThrLeuThrGlnGlnLutProLysArg 83
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
279 CCGCTTCACATGGAAGCGCTGAGAGCTTGCAATATGAAAGAGTTCG 328
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
83 ArgLeuThrThrLysProGlnAspHisAsnMetLysLysValArgL 100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
329 TCCTTCACAAACATGCTGCTCCAGATGGTCTCTATACAAATGCG 378
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
100 euProSerLysHisLileThrLeuProAspValValLeuThrAsnAsnAla 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
379 GAGCGATGACAGAGCTCTCTCTATTCATGCTGCTGCTCTCTATGA 428
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
117 AspGlyMetCysGlnValSerPheTyrSerAsnAlaValIleSerTyrAs 133
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
429 TGCGACATCTTTGGCTACCACTGCGCATCTACAGAGTGCATGACGA 478
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
133 polySerIleMetThrLeuProAlaIleTyrLysSerAlaCysLysL 150
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
479 TTGAGGTGAAGCACTTCCCATTTGACACAGAAATTCACCATGAGTTT 528
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
150 IeValLysHisThrPheAspGlnGlnAsnGlyThrMetLysPhe 166
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
529 CCGTATGAGCTACAGACCGTACTGAGATTGACTGCTGCTCAAAAGTGA 578
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
167 ArgSerThrPheTyrAspArgThrGlnIleAspLeuValLeuLysSerG 183
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
579 TGTGGCAGTCTGGATGATCTACACACCGGCGGAGTGGAGCATCATCG 628
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
183 uValAlaSerLeuAspAspPheThrProSerLysLutProspLleValA 200
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
629 CACTGGCAGCGCGACGACAGAGAGACCCAGAGACTCCACCTATGTGGAC 678
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 IeLeuProGlyArgArgAsnGlnAspProAspSerThrTyrValAsp 216
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
679 ATTCACCTATGACTTATCTGCTGCCAAACCACTCTTACACTATCA 728
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
217 IeThrTyrAspPheIleIleArgArgLysProLeuPheTyrThrIleAs 233
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
729 CCTCATATCCCTGGCTACTCATCACTGCTGCGTCCATCCCTGCTTCT 778
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
233 nLeuIleIleProCysLysLeuIleThrSerLeuAlaIleLeuValPhe 250
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
779 ACCTGGCCTCAGACTGTGTGAAAGATGACACTTGTATTTCTGTGCTG 828
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 TyrLeuProSerAspCysGlyGlnLysMetThrLeuCysIleSerValLeu 266

```

```

829 CTAGCATCAGCGTGTCTGCTGCTCATCTCCAGATTGACCTCCAC 878
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267 LeuAlaIleThrValPheLeuLeuIleSerLysIleValProProth 283
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
879 CTCCCTCAGTGTACCGCTGGGCGGAGATCCTCATGTTTCCATGGTGC 928
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
283 rSerLeuAspValProLeuValGlyLysTyrLeuMetPheThrMetVal 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
929 TAATCATCTTCCATGCTGACCGAGCTGTGCTGCTCATATGTCACACC 978
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 euValThrPheSerIleValThrSerValCysValLeuAsnValHisHis 316
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
979 CGCTGGCTTACACGACACCACTGAGCGCCCTGCGTCAGCGCTCCCT 1028
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
317 ArgSerProThrThrHisThrMetProProThrPValAlaThrLeuPhe 333
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1029 GAGAAAGTGGCCACCGCTGCTCTGCGACGACGACCGACCGCGTGG 1078
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
333 uArgLysLeuProAlaLeuLeuPheMetLysGlnProGlnAsnGlyAs 350
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1079 CAGTCAGGCTGCTGCGCTGAGAGGCGCAGCAGAGACCTGAGAGCGAG 1128
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 IeArgGlnArgLeuArgGlnArgGlnThrGlnGluArgAlaAlaAla 366
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1129 GCG...GTTTCTTCCCTGGAAGCTCCTCGCGCTGACCCATGTACTGCTT 1175
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
367 AlaThrLeuPheLeuArgAlaGlyAlaArgAla....CysAlaCysTyr 381
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1176 TGTCAACCT....GCATCACTGCAGGGCTTGAGCTGGGCTTCCGAG 1219
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 rAlaAsnProGlyAlaAlaLysAlaGlnLysAlaGlnLysMetLys...TyrArg 396
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1220 CTGAGCGCATGACAGCGCGCGCGCGCTGTGGGCGCATGACAGCTGT 1269
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
397...GluArgGlnLysGlnLysProAsp...ProProAlaIleProCysGlyCys 411
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1270 GGCCTTCGCGGAAAGACAGTGAATGCGCTTCACTTTCGACACATGCG 1319
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
412 GlyLeuGlnGlnAlaValGlnGlyValArgPheIleAlaAspHisMetLar 428
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1320 AAGTGAAGATGATGACAGAGTGTGAGGAGGAGCTGGAATATGCTGCCA 1369
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 gSerGlnAspAspAspGlnSerValSerGlnAspThrLysTyrValAla 445
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1370 TGTGATGACCGCGCTGCTGTGATGATCTTGTCTGTGTGTGTCTTT 1419
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 eValIleAspArgLeuPheLeuThrPheIlePheValPheValCysValPhe 461
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1420 GGGACCGTGGCATGTTCTCGACGCTCTCTTCAGAACTACACTGCGCAC 1469
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
462 GlyThrValGlyMetPheLeuGlnProLeuPheGlnAsnTyrAlaThrAs 478
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1470 TACCTTCTCCACCTGACAGCATCAGCTCCAGCTCCAG 1509
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 nSerLeuLeuGlnLeuGlnGlyGlnLysThrProThrSerLys 491
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq\_name: p1r2:A39218

## seq\_documentation\_block:

nicotinic acetylcholine receptor chain non-alpha-3 chain precursor - chicken (fragmen  
 C:Species: Gallus gallus (chicken)  
 C:date: 30-Aug-1991 #sequence-revision 30-Aug-1991 #text-change 30-May-1997  
 C:accession: A39218  
 J:Bio1. Chem. 265, 17560-17567, 1990  
 A:title: alpha5, alpha3, and non-alpha3. Three clustered avian genes encoding neurona  
 A:reference number: A39218; MUID:91009210  
 A:accession: A39218  
 A:status: preliminary  
 A:molecule type: DNA  
 A:residues: 1-470 <C00>  
 A:cross-references: GB:J05642  
 C:superfamily: acetylcholine receptor

C:Keywords: neurotransmitter receptor; transmembrane protein

alignment\_scores:  
 Quality: 1743.00 Length: 476  
 Ratio: 4.231 Gaps: 4  
 Percent Similarity: 86.555 Percent Identity: 69.748

alignment\_block:  
 US-07-938-154-10 x A39218 ..

Align seq 1/1 to: A39218 from: 1 to: 470

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88 GACACAGAGAGAGCGCTAGTGGAGCATCTCTATGATCCCTCCGCTATTA 137
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5 AspalaglululsleuMetIasnHisIleuSerProAsparglyTyr 21
138 CAAGCTGATTCGTCAGCTACTAACGGCTCTGAGCTGGTACTGTACAG 187
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
21 nLysLeuIleArgProAlaValAsnSerSerGlnLeuValSerIleGlu 38
188 TCATGGTATCATTCGCTCAGCTCATTAAGTTCGACGAGCGAGCAGATC 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
38 euGlnValSerLeuAlaGlnIleuIleSerValAsnGlnArgGlnIle 54
238 ATGACCAACCATGTCTGGCTGACCCAGAGGTGGAAAGATTACCGCTCAC 287
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
55 MetThrIasnValIlePheAsnGlnGlnIlePheAspIleArgLeuAl 71
288 ATGGAAGCTCGAGACTCGACATATGAAGAAGTCGCGCTCCCTTCCA 337
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
71 atPlyPheProSerAspIleArgGlnIleAsnMetLeuArgIleProAla 88
338 AACACATCTGCTCCAGATGGTCTTATACAAACATGCTGACGGCAG 387
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
88 yshHisIleTleuProAspIleValLeuIleYrAsnAsnAlaAspGlyThr 104
388 TAGAAGTCTCTTATTCATTCATGCTGCTGCTCCATGATGACAGCAT 437
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
105 TyrGlnValSerLeuIleYrIasnAlaIleValGlnAsnAsnGlySerI 121
438 CTTTGGGCTACCACTGCTGCTACCAAGATGATGATGAGTGA 487
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 eaGlyTleuProProAlaIleTyrIleYrSerAlaGlyIleGlnValI 138
488 AGGACTCCCATTTGACCGACAGATTTGCACATGAAGTTTGGCTCATG 537
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
138 yshHisPheProPheAspGlnGlnAsnGlyThrLeuYsPheArgSerTrp 154
538 ACCTAGACCGTACTGAGATTGACGTGGTCTCAAAAGATGATGGCCAG 587
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
155 ThrTyrAspHisThrGlnIleAspMetValLeuYsThrSerMetAla 171
588 TCTGGAGTCTTCAACCCGAGGAGTGGGATGACATCATGCACTCCAG 637
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
171 rMetAspAspPheThrProSerGlyGlnIlePheValAlaIleuPro 188
638 GCCGACGACGAGAGAACCCAGACGACTCCACTATGTGACATCACTAT 687
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
188 LysArgGlyThrGlnAsnProLeuAspProAsnIleValAlaPheValThr 204
688 GACTGTATCATTCGTCGCAACCACTCTTACATATCAACCTCATCAT 737
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
205 AspPheIleIleuYsArgIleYsProLeuPheTyrThrIleAsnLeuIle 221
738 CCCCTGGTACTCATCACTCGCTGGGCATCTGCTCTTACCTGACCTG 787
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
221 eProCysValLeuIleThrSerLeuAlaIleLeuValPheTyrLeuPro 238
788 CAGACTGTGTGAAAAGATACACTTTGTATTTCTGTGCTGCTAGCAGCT 837
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
238 eAspCysGlyGlnYsMetThrIleuYsIleSerValLeuLeuAlaLeu 254

```

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838 ACGGTTCCCTGCTGCTCATTCGAAAGATTGGCTCCACCTCCGTCGA 887
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255 ThrValPheLeuLeuIleSerIleValIleProIleHisSerLeuAs 271
888 TGTACCGCTGTGGGCAAGTACCTCATGTTTACATGGTGTAGTACCT 937
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
271 pAlaProLeuIleGlyIleYsTyrLeuMetPheThrMetValLeuValThr 288
938 TCTCATGCTCCACGAGCGTGTGTCATGATGTCACACCGCTGCGCT 987
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
288 HisSerIleValThrSerValCysValLeuAsnValHisHisArgSerPro 304
988 ACCACACACCATGAGCCCGCTGGGTCAAGGTGTCTCTGAGAGAGCT 1037
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
305 SerThrHisThrMetProThrPheValIleuValPheLeuGlnArgLe 321
1038 GCCACCCCTGCTTCTCCGACAGCAGCCAGCCACCGCTGTGACGTCAGC 1087
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
321 nProAlaTyrLeuPheMetLysArgProGlnAsnAsnSerProArgGln 338
1088 GTCTGCGCTTGAAGAGGCGCCAGCAGAGCGTGAAGGCGGCTTTTC 1137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
338 yAsProAlaAsnGlyIleYsThrArg..... 346
1138 TTCCTGGAAGGCTCTGCGCTGACCATGT.....AC 1169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
347 ..AlaGlnAsnLeuGlyMetAspProAlaAspPheTyrLysAsnSerThr 362
1170 CTGCTTTGTCACACCTGCATCAGTCAG..... 1197
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
362 TyrIlePheValAsnThrAlaSerAlaIleYsTyrAspMetLysIleThr 379
1198 ..GCCTGCTGGGCTTCCGAGCTGAGCCCATGACCGCGCGCGG 1245
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379 sPThrLeuAspAsnValSerSerHisGlnAspPheArgLeuArgThrIle 395
1246 CGCTGTGTGGGCGCATGACGTGTGCGCTCCGAGAGCATGATGATGGCT 1295
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
396 ThrIleYsPheSerPro.....GlnValGlnGlnAlaIleAspGlyVal 409
1296 ACGCTTCATTCGCGACACATGCGAAGTGAAGATGATGATGACAGATGTA 1345
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
409 IserPheIleAlaGlnHisMetLysSerAspAspAsnAspGlnSerVal 426
1346 GGGAGGATGGAATACGTTGCCATGATGATGACCGGCTGTTCTGTGG 1395
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
426 IeGlnAspIlePlyIleValAlaIleMetValAlaAspArgLeuPheLeuTrp 442
1396 ATCTTGTCTTGTCTGTCTTGTGGACCGTGGCATGTTCTGTACAGCC 1445
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
443 IlePheValLeuValCysValLeuGlyThrValGlyLeuPheLeuGlnPr 459
1446 TCTCTTCCGAACTACACGCGCATAC 1473
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
459 oLeuPheGlnAsnHisIleAlaIleThr 468

```

seq\_name: p1r2:S14703

seq\_documentation\_block:

nicotinic acetylcholine receptor beta-2 chain - goldfish (fragment)

C:Species: Carassius auratus (goldfish)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999

C:Accession: S14703

R:Heber, V.; Bouchev, J.; Agranoff, B.W.; Goldman, D.

Nucleic Acids Res. 18, 5307, 1990

A:Title: Nucleotide and deduced amino acid sequence of the goldfish neural nicotinic

A:Reference number: S14703; MUID:90384858

A:Accession: S14703

A:Molecule type: mRNA

A:Residues: 1-459 <HIE>

A:Cross-references: EMBL:X54052; MID:962576; PIDN:CAA37986.1; PTD:9833601

C:Superfamily: acetylcholine receptor

C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra

## alignment\_scores:

Quality: 1660.50 Length: 470  
 Ratio: 4.269 Gaps: 5  
 Percent Similarity: 82.766 Percent Identity: 67.021

## alignment\_block:

US-07-938-154-10 x SI4703

Align seg 1/1 to: SI4703 from: 1 to: 459

```

109 GAGCATCTCTTAGATCCCTCCGCTATATACAAAGCTGATTGCTCCAGCTAC 158
    ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
4  AspPheLeuLeuGlyProGluArgTyrAsnLysLeuIleArgProAlaVal 20
159 TAAAGCGCTGAGCTGTGACTGCTACAGCTCATGCTATCATTTGGCGTCAGC 208
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
20  LAsnLysSerGlnGlnValThrIleGlyIleLysValSerLeuAlaGlnL 37
209 TCATTAGTGTGACGAGCGGAGACAGATCATGACCAATGTCTGGCTG 258
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
37  euIleSerValAsnGluArgGlnIleMetThrAsnValThrPheLeu 53
259 ACCGAGAGTGGGAAGATTACCGCCTCACATGAGAGCTGAGGAGCTTGA 308
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
54  ThrGlnGluTrpThrAspTyrArgLeuValTrpAspProAsnGluTyrGl 70
309 CAATATGAGAAAGTCCGGCTCCCTCCAAACACATCTGGCTCCAGATG 358
    ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
70  uGlyIleLysLysLeuArgIleProSerGlnHisIleTrpLeuProAspI 87
359 TGGTTCTATACAAAGTGTGACGGGATGAGAGCTGCTCTCTATTCG 408
    ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
87  IeValLeuTyrAsnAsnAlaAspGlyValTyrGluValSerPheTyrG 103
409 AATGCTGTGCTCTCTATGATGAGCATCTTTGGCTACCACTGCCAT 458
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
104  AsnAlaValAlaSerAsnThrGlyAspIlePheTrpLeuProProAlaI 120
459 CTACAGAGTGTGATGCAAGATTGAGTGAAGCACTCCCATTTGAGCAGC 508
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
120  eTyrLysSerAlaCysAlaIleGluValArgAsnPheProPheAspGln 137
509 AGAATTGCACCATGAAGTTTCGCTCATGAGCTAGACCGTACTGAGATT 558
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
137  LAsnGlyThrLeuLysPheArgSerTrpThrTyrAspArgThrGluLeu 153
559 GACTGTGCTCTCAAAAGTATGATGTGGCAGTGTGAGTCTACACCCAG 608
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
154  AspLeuValLeuThrSerAspPheAlaSerArgAspAspTyrThrPro 170
609 CGGGAGTGGGACATATGCGACTGCGAGCGGACGACCAAGAGAACCCAG 658
    ||||| ::::: ||||| ::::: ||||| ::::: |||||
170  rGlyGluTrpAspIleValSerLeuProGlyArgLysAsnGluAspPro 187
659 ACGACTCCACTATGTGAGCATCATCTATGACTTTCATCTGCTCCCAA 708
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187  snAspLeuThrTyrLeuAspIleThrTyrAspPheValIleLysAspGly 203
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  R:Kurayakov, A.; Anand, R.
  submitted to the EMBL Data Library, February 1996
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  submitted to the EMBL Data Library, June 1996
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441 euGluSerAspAspArgAspGlnSerValIleGluAspTrpLysPheVal 457
1366 GCCATGTGTATGACCGCGCTGTCTCTGTGATCTTTGCTTTGCTGTGT 1415
458 AlameValValAspArgLeuPheLeuTrpValPheValAlaCysIle 474
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C:Accession: A30992
R:isenberg, K.E.; Meyer, G.E.
J. Neurochem. 52, 988-991, 1989
A:Title: Cloning of a putative neuronal nicotinic acetylcholine receptor subunit.
A:Reference number: A30992; MUID:89140821
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A>Status: preliminary
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1188 ..... 1188
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444 eTrpGlySerCysProProProlLysSerSerSerGlyAlaProMetLeu 460
|||||
1189 .....TCAGTGCAG..... 1197
|||||
461 IleLysAlaArgSerLeuSerValGlnHisValProSerSerGlnGluAl 477
|||||
1197 ..... 1197
|||||
477 aAlaGluAspGlyIleArgCysArgSerArgSerIleGlnTrpCysVal 494
|||||
1198 .....GCTTGCTGGGCTTCCGAGCTGAGCCACCA... 1233
|||||
494 eGlnAspGlyAlaIleAspSerLeuAlaAspSerLysProThrSerSerPro 510
|||||
1234 .....GCGGCGCGGCGCGC.....TCTGTGG 1256
|||||
511 ThrSerLeuLysAlaArgProSerGlnLeuProValSerAspGlnAlaSe 527
|||||
1257 GCCATGCACTGTGGCTCCGGAA..... 1281
|||||
527 rProCysLysCysThrCysGluProSerProValSerProValThrV 544
|||||
1281 ..... 1281
|||||
544 aLeuLysAlaGlyThrLysAlaProProGlnHisLeuProLeuSer 560
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1282 .....GCAGTGAAGCGGTACCGCTTCATTTGCGAGACACAT 1316
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561 ProAlaLeuThrArgAlaValAlaGlnGlyValGlnTrpIleAlaAspHisI 577
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1317 GCGAAGTGAAGATGATGACAGAGTGTGAGGAGACTGGAATACGTTG 1366
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577 uLysAlaGluAspThrAspPheSerValLysGluAspTrpTrpValAla 594
|||||
1367 CCATGATGATGACCGCCCTGTCCTGTGATCTTTGTTGTGCTGTC 1416
|||||
594 IeMetValIleAspArgIlePheLeuTrpMetPheIleIleValCysLeu 610
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1417 TTTGGACCGCTCGCATGTCTCTGCAAGCT 1446
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611 LeuGlyThrValGlyLeuPheLeuProPro 620
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seq_name: p1r2:JC4021

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seq_documentation_block:
nicotinic acetylcholine receptor alpha-4 chain, neuronal - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C:Accession: J04021; S55471
R:Monteggia, L.M.; Gopalakrishnan, M.; Touma, E.; Idler, K.B.; Arneric, S.P
Gene 155, 189-193, 1995
A:Title: Cloning and transient expression of genes encoding the human alpha 4 and bet
A:Reference number: J04021; MUID:95237608
A:Accession: J04021
A:Molecule type: mRNA
A:Residues: 1-627 <MON>
A:Cross-references: GB:J35901; NID:g755647; P1DN:AAA64743.1; P1D:g755648
R:Maniaki, A.; Remondos, M.; Tzartos, S.
submitted to the EMBL Data Library, May 1995
A:Description: Molecular cloning of human neuronal nicotinic acetylcholine receptor 4
A:Reference number: S55471
A:Accession: S55471
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 26-627 <MAN>
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C:Genetics:
A:Gene: GDB:CHRNA4
A:Cross-references: GDB:128169; OMIM:118504
A:Map position: 20q13.2-20q13.3
C:Superfamily: acetylcholine receptor
C:Keywords: ion channel; neurotransmitter receptor; postsynaptic membrane; transmembr

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alignment_scores:
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Ratio: 3.238 Gaps: 14
Percent Similarity: 59.520 Percent Identity: 42.720

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alignment_block:
US-07-938-154-10 x JC4021 ..

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Align seg 1/1 to: JC4021 from: 1 to: 627

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36 GGGCGCTTCAGCTTCAGCTTCTTGGCTGCTGCTGAGGGTTTGGGA 84
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7 gLysAlaProArgLeuLeuProProLeuLeuLeuLeuGly.ThrGly 23
|||||
85 .....ACTGACACAGAGAGCGG 102
|||||
23 eUeuArgAlaSerSerHisValGluThrArgAlaIleAlaGluArg 39
|||||
103 CTAGTGAGACATCTTTCATCCCTCCGCTATACAGAGATTCGTC 152
|||||
40 LeuLeuLysLeuPhe.....SerGlyTrpAsnLysTrpSerArgPr 54
|||||
153 AGCTAAACGCTGTGAGCTGGTACTGATACAGCTCATGATATCATGG 202
|||||
54 oValAlaAsnIleSerAspValValLeuValArgPheGlyLeuSerIleA 71
|||||
203 CTGAGTCTTGTAGTGCACGAGCGAGACAGATCATGACACCAATGTC 252
|||||
71 IeGlnLeuLeuAspValAspGlyLysAsnGlnMetCThrThrAsnVal 87
|||||

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816 TATTTCTGTCTAGACAGCTACGGTGTTCCTGCTCATCTCCAGA 865
|||||
268 SLLESEVALLLEULEUSERLEUTHRALPHEULEUVALILLETHGLUT 285
|||||
866 TTGGCCCTCCACCTCCCTGATGTAACCGCTGGTGGCAAGTACCTCAG 915
|||||
285 HTLEPROSEFTHSERLEUVALILEPROLEULEGLEUTYRLEULEU 301
|||||
916 TTTACCATGTCTAGTACCTTCCTCCACGTCACACGCTGTGTGCT 965
|||||
302 PHEITHMETILLEPHEVALTHREUSERILLEVALILLETHRALPHEVALLE 318
|||||
966 CAATGTGCACACCGCTCGCTACACGACACCATGACCCCTGGGTCA 1015
|||||
318 UASNVAILHSTYRATGYTHPROMETHRHSTHMETPROSETRIPYALA 335
|||||
1016 AGGTGCTTCTCTGAGAGAGTCCACCCCTGCTCTTCGTGACAGACCA 1065
|||||
335 TGYTHRALPHEULARGALALEUPROARGVALMETLEUMETARGPRO 351
|||||
1065 ..... 1065
352 LLEASPLEUSERGLUSERSERGLYSGLYGLYLLEALAGLYSE 368
|||||
1066 .....CGCCACCGCTGTGCTGACGTCACGCTGCGCTTGAGA 1102
|||||
368 RSEGLYTHRGLYGLYARGGLYALAGLYLYSGLYMETLYSERS 385
|||||
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|||||
385 ERALSERGLNGLYALAMETASNSERLEULUPHEGLYGLYLYS 401
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1153 GCGGCT.....GACCATGTACTGCTTGTGTCAACCTGC 1187
|||||
402 ALAILEUGLUGLYLYSLYSGLYCYSPROCYSHISPROILEUGSL 418
|||||
1188 ATCAGTGCAGGGCTTGCTGGGCTTTCGAGCTGAG.....CCCACTG 1221
|||||
418 UALALEGLUGLYASPCYSGLYLYSVALSERARGINLEUTHRPROGLNA 435
|||||
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435 LALLEASNRHVALVALTHRPHESEVALVALSERPROGUILLELYSGLN 451
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1282 GCAGTGGATGCGCTACGCTTCATTGCGGACACATGCGAAGTGA 1331
|||||
452 ALAILEGLUSERVALYSTYRILEALAGLUSNMETARSERARGASNYL 468
|||||
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468 SALALYSGLUVALGLUASPSAPTRIPYSTYRVALALAMETVALILLESPA 485
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1382 GCGTGTCTCTGGATCTTGTGTTGCTGTCTGTTGGAGCGTGGC 1431
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485 RGLLEPHELEUTHRALPHEVALLEVALCYSVALLEUGLYTHLEUGLY 501
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502 LEUPHELEUGLNPHELEU 507
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acetylcholine receptor alpha chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C:Accession: S60589
R:Criado, M.; Alamo, L.; Navarro, A.
Neurochem. Res. 17, 281-287, 1992
A>Title: Primary structure of an agonist binding subunit of the nicotinic acetylcholine
A:Reference number: S60589; MUID:92319195
A:Accession: S60589
A:Status: preliminary

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A:Molecule type: mRNA
A:Residues: 1-495 <CRI>
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C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-495/Product: acetylcholine receptor alpha chain #status predicted <MAT>

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Ratio: 3.175 Gaps: 9
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US-07-938-154-10 x S60589 ..

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1 MetAlaArgSerArgLeuArgArgLeuLeuLeuLeuLeuP 17
63 GCTGTCTACAGGGGTTTGGAACTGACACAGAGAGCGGCTAGTGAGC 112
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17 OValAlaSer.....ThSerAspAlaGluHisArgLeuPheGlu 31
113 ATCTCTTAGATCCCTCCCGCTATTAACAGCTGATTCGCTCAGCTACTAC 162
|||||
31 rLeuPheGluAsp.....TyrAsnGluIleLeuArgProValAlaAsn 45
163 GGCCTGTGAGCTGTGACTGTACAGCTCATGTATCACTTGGCTGAGTCAT 212
|||||
46 ValSerAspProValIleLeuGlnPheGluValSerMetSerIleuVal 62
213 TAGTGTGACAGAGCGGAGAGATGACACCAATGTCGTGAGTACC 262
|||||
62 llyValAspGluValAlaAsnGlnIleMetGluThrAsnLeuTrpLeuLysG 79
263 AGAGTGGAGACATTACCGGCTTCACATGAGAGCTGAGAGCTTCGACAAAT 312
|||||
79 lIleTrpAsnAspTyrIlyLeuLysTrpAsnProSerAspTyrAspGly 95
313 ATGAGAAAGTCCGGCTCCCTCCAAACACATGCTGCCAGATGAGT 362
|||||
96 AlaGluPheMetArgValProAlaGluLysIleTrpLysProSplIeVal 112
112 lLeuTyrAsnAsnAlaValAlaGlyAspPheGlnValAspAspLysThrLysA 129
413 CTGTGTCCTCATGATGAGCAGCATCTTTGGCTACACCTGCATCTAC 462
|||||
129 lAlaLeuLysTyrThrGlyGluValThrTrpIleProAlaIlePhe 145
463 AAGAGTGCATGCAAGTGTGAGTGAAGCACTCCCAATTGACGAGAGAA 512
|||||
146 LysSerSerCysLysIleAspValIleThrTyrPheProPheAspTyrGlnAs 162
513 TTGCACCATGAAGTTTGCCTCATGAGCACTAGACGCTACTGATGATGACC 562
|||||
162 nCysThrMetLysPheGlySerTrpSerTyrAspLysAlaLysIleSpl 179
563 TGGTGTCAAAAGTCAATGTGGCCAGTCTGTGATCTTACACACCGAGGG 612
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179 euValLeuIleGlySerSerMetAsnLeuLysAspTyrTrpGluSerGly 195
613 GAGTGGAGCATGATGCGACACTGCCAGGCGGACGACAGAG.....AA 653
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196 GluTrpAlaIleIleLysAlaProGlyTyrLysHisAspIleLysTyrAs 212
654 CCCAGACACTCCACCTATGTGACATCACCTATGACTCATGCTGTC 703
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212 nCysCysGluGluIleTyrProAspIleThrTyrSerLeuTyrIleArg 229  
704 GCAAAACCACTTCTTACACTATCACTACATCACTCCCTGGTACTCATC 753  
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229 rglLeuProLeuPheTyrThrIleAsnLeuIleIleProCysLeuLeuIle 245  
754 ACCTCGCTGGCCATCCTGGTCTTCTTACCTGCCCTCAGACTGTGTGAAA 803  
11 |||||  
246 SerPheLeuThrValLeuValPheTyrLeuProSerAspCysGlyIle 262  
804 GATGACACTTTGATTCTGTCTGTGAGACATCACTGCTCTCTCTGCTGC 853  
11 |||||  
262 sValThrLeuCysIleSerValLeuLeuSerLeuThrValPheLeuLeu 279  
854 TCATCTCCAGATTTGCTCCACCTCCCTCGATGATGACCTGTGTGGC 903  
11 |||||  
279 alIleThrGluThrIleProSerThrSerLeuValIleProLeuIleGly 295  
904 AAGTACCTCATGTTTACCATGTTGCTAGTACCTTCTCATCTGTACCAG 953  
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296 GluTyrLeuLeuPheThrMetIlePheValThrLeuSerIleValIleThr 312  
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312 rValPheValLeuAsnValHisTyrThrProThrThrHisThrMetP 329  
1004 CCCCTGGGTCAAGGTGTCTTCTGTGAGAACCTGCCACCTGTCTTTC 1053  
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329 rValThrValIleThrIlePheLeuAsnLeuLeuProArgValMetPhe 345  
1054 CTG.....CAGCAGCCACGCCACCG 1073  
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346 MetThrArgProAlaSerAsnGluGlyAsnThrGlnArgProArgPropH 362  
1074 CTGTGCACCTGACCGCTGTGCTGCTGAGAGGCGCAGCGAGCGTGAG 1123  
11 |||||  
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1124 GCGAGCGGCTTCTTCCGTGAAGTCTGCGGCTGACCCATGTACCTGC 1173  
11 |||||  
377 ..GluSerLysValCysLysGluGly.....TyrProCysGln... 388  
1174 TTTGTCAACCCCTGCATGAGTGCAGGCTGTGGCTGGG..... 1209  
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389 .....AspGlyLeuCysGlyTyrCysHisHisAr 398  
1210 .....GCTTCCAGCTGAGCCCACTGCAGCGGCGCCG 1243  
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398 gArgAlaLysIleSerAsnPheSerAlaAsnLeuThrArgSerSerSers 415  
1244 GCGCGCTGTG.....GGGCCATGCAGCTGTGGCCTC 1275  
11 |||||  
415 eArgIleSerValAspAlaValLeuSerLeuSerAlaLeuSerProGluIle 431  
1276 CGGAGAGCAGTGAATGAGGAGAGTGAATACGTTGCCATGGTGA 1375  
11 |||||  
432 LysGluAlaIleGlnSerValLysTyrIleAlaGluAsnMetLysAlaG 448  
1326 GGATGATGACCAAGTGAAGTGAAGAGTGAATACGTTGCCATGGTGA 1375  
11 |||||  
448 nAsnGluAlaLysGluIleGlnAspAspTyrLysTyrValAlaMetValI 465  
1376 TCGACCGCGCTTCTCTGTGATCTTGTCTGTGTCTGTGTCTTGTGGACC 1425  
11 |||||  
465 leaSpArgIlePheLeuThrValPheIleLeuValCysIleLeuGlyThr 481  
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482 AlaGlyLeuPheLeuGlnProLeu 489

OM of: US-07-938-154-10 to: SwissProt\_39:\* out\_format : pfs  
 Date: Oct 16, 2001 6:17 AM

About: Results were produced by the Gencore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

## Command line parameters:

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 -GAPXT=4.000 -MINMATCH=0.100 -LOOPEC=0.000 -LOOPEXT=0.000  
 -GAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
 -DELOP=6.000 -DELEXT=7.000 -STAR=1 -MATH=x-biosubm2  
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 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
 -NORM\_ext -MINLEN=0 -MAXLEN=200000000 -USER=5981193\_cgn1.1\_37  
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## Search information block:

Query: US-07-938-154-10  
 Query length: 1512  
 Database: SwissProt\_39:\*  
 Database sequences: 93435  
 Database length: 34255486  
 Search time (sec): 42.450000

## score\_list:

Sequence	Strd Orig	ZScore	EScore	len	Documentation
SwissProt_39:ACHN_RAT + 2624.50 3124.74	4.2e-167	500	1	P12390	rattus norvegicus (rat)
SwissProt_39:ACHN_HUMAN + 2432.00 2895.19	2.5e-154	502	1	P17787	homo sapiens (human)
SwissProt_39:ACHN_CHICK + 2129.00 2534.13	3.4e-134	491	1	P09484	gallus gallus (chick)
SwissProt_39:ACHN_CHICK + 1743.00 2074.30	1.4e-108	470	1	P13933	gallus gallus (chick)
SwissProt_39:ACHN_CARAU + 1660.50 1976.14	4.3e-103	459	1	P13937	carassius auratus (g)
SwissProt_39:ACHN_HUMAN + 1630.00 1939.08	4.6e-101	498	1	P13926	homo sapiens (human)
SwissProt_39:ACHN_RAT + 1594.00 1896.21	1.1e-98	495	1	P12392	rattus norvegicus (rat)
SwissProt_39:ACHN_CHICK + 1221.00 1454.52	4.3e-74	528	1	P09480	gallus gallus (chick)
SwissProt_39:ACHN_HUMAN + 1221.00 1450.92	6.7e-74	529	1	P01582	homo sapiens (human)
SwissProt_39:ACHN_RAT + 1210.00 1436.30	7.7e-73	630	1	P09483	rattus norvegicus (rat)
SwissProt_39:ACHN_HUMAN + 1205.00 1439.15	7.8e-73	511	1	P12389	rattus norvegicus (rat)
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SwissProt_39:ACHN_SCORCA + 1054.00 1251.37	8.4e-63	557	1	P23414	schistocerca gregaria
SwissProt_39:ACHN_DROME + 1032.50 1225.45	2.2e-61	576	1	P17644	drosophila melanogast
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SwissProt_39:ACHN_MOUSE + 1016.50 1208.37	2.5e-60	457	1	P04756	mus musculus (mouse)
SwissProt_39:ACHN_BOVIN + 1014.50 1205.99	3.4e-60	457	1	P02709	bos taurus (bovine)
SwissProt_39:ACHN_RAT + 1014.50 1205.99	3.4e-60	457	1	P02709	bos taurus (bovine)
SwissProt_39:ACHN_TORCA + 1003.00 1191.62	8.0e-60	464	1	P25108	rattus norvegicus (rat)
SwissProt_39:ACHN_MOUSE + 1003.00 1191.62	8.0e-60	464	1	P25108	rattus norvegicus (rat)
SwissProt_39:ACHN_CHICK + 1003.00 1191.48	2.0e-59	493	1	P12391	rattus norvegicus (rat)
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SwissProt_39:ACHN_HUMAN + 995.00 1184.51	5.4e-59	458	1	P00590	homo sapiens (human)
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 SwissProt\_39:ACHN\_CARAU + 991.50 1178.47 1.2e-58 462 1 P13908 carassius auratus  
 SwissProt\_39:ACHN\_CHICK + 991.00 1177.99 1.2e-58 456 1 P09479 gallus gallus (ch)  
 SwissProt\_39:ACHN\_RAT + 987.00 1173.30 2.3e-58 452 1 P0420 rattus norvegicus (r

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seq\_documentation\_block:  
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 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-2 CHAIN PRECURSOR (NON-  
 DE ALPHA 1) (N-ALPHA 1).  
 GN CHRNA2 OR ACRB2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90166479; PubMed=3272154;  
 RA Boulter J., Connolly J., Deneris E.S., Goldman D.J., Heinemann S.F.,  
 RA Patrick J., Heinemann S.;  
 RT "Primary structure and expression of beta 2: a novel subunit of  
 RT neuronal nicotinic acetylcholine receptors.";  
 RL Neuron 1:45-54(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041184; PubMed=2444984;  
 RA Boulter J., Connolly J., Deneris E.S., Goldman D.J., Heinemann S.F.,  
 RA Patrick J.;  
 RT "Functional expression of two neuronal nicotinic acetylcholine  
 RT receptors from cDNA clones identifies a gene family";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7763-7767(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Hartley M.;  
 RL Submitted (Nov-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN  
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND  
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA  
 CC MEMBRANE.  
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES  
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). BETA-2 SUBUNIT CAN BE  
 CC COMBINED TO ALPHA-2, ALPHA-3, OR ALPHA-4 SUBUNITS TO GIVE RISE TO  
 CC FUNCTIONAL RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST REGIONS OF THE CNS.  
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
 CC -----

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EMBL: L31622; AAC8724.1;  
 PIR: J0174; J0174.  
 DR InterPro: IPR001175;  
 DR InterPro: IPR002394;  
 DR Pfam: PF00065; neur\_chan. 1;  
 DR PRINTS: PR00252; NRIONCHANNEL.  
 DR PRINTS: PR00254; NICOTINIC.  
 DR POSTSITE: PR00236; NEUROTFR\_ION\_CHANNEL. 1;  
 KW Transmembrane; Multigene family.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 500 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,  
 FT BETA-2 CHAIN.

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FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 267 287 POTENTIAL.
FT TRANSMEM 300 320 POTENTIAL.
FT DOMAIN 321 438 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 459 479 POTENTIAL.
FT DISULFID 154 168 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 500 AA; 56908 MW; 54C007A48225931C CRC64;

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  Percent Similarity: 99.600      Percent Identity: 99.400

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alignment\_block:

US-07-938-154-10 x ACHN\_RAT ..

Align seg 1/1 to: ACHN\_RAT from: 1 to: 500

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1 METALIGLYHISSETRASMERMETALALEUPHESERLEULEUTR 17
63 GCTGTGCTCAGGGGTTTGGAACTGACACAGAGAGCGGCTAGTGAGC 112
17 PLEUCYSSERGLYVALLEUGLYTHRSPHRCGLDGLUARGLEUVALGLUH 34
113 ATCTCTTACATCCCTCCGCTTATACAGACGTGATCGTCCAGCTACTAC 162
34 ILEULEUNSPROSERATRGYRASNLYSLEULILEARGPROALATHRASN 50
163 GGCTCGAGCTGTGACTGTACAGCTCATGATGATTCATGCTCAGCTCAT 212
51 GLYSERGLULEUVALTHRVALGLINLEUWEVALSERLEUALAGINLEUL 67
213 TAGTGTGACGAGCGGAGACAGATCATGACACCAACATGTCTGGCTGACC 262
67 ESEERVALHISGLUARGGLUGINILEMECTHTRASNVALTRPHEUTHRG 84
263 ACGAGGGAAGATTACCGCTCATGAGAGCGTGAAGCTTGAGACTTGACAT 312
84 INGLUTRIPGLUNSPYRARGLEUTHRTTRPILYSPROGLUASPRHEASPRSN 100
313 ATGAGAAAGTCCGCTCCCTTCAACAACATCTGGCTCCAGATGTGGT 362
101 METLYSLYSVALARGLEUPROSERLYSHISLETTRPLEUPROASPRVALVA 117
363 TCTATACAAATGCTGACGCGATGATGAGATGCTCTTATTCCAATG 412
117 LEUTYRASNASNALASPGLYMETYRGLUVALSERPHERYSEERSNA 134
413 CTGTGCTCCCTATGATGAGCAATCTTGGCTAACCCATGCCATCTAC 462
134 IVALVALSERLYRASPGLYSERILEPHERPLEUPROALALEUYR 150
463 AAGAGTCATGCAAGATTGAGGTGAAGCACTTCCATTGACGACGAA 512
151 LYSSEIRALACYLSYILLEGLIUALYSHISHPHEOPHEASPRGLINGLNAS 167
513 TTGCACCATGAGTTGCTGCTATGAGCTAGACCGTACTGAGATTGACC 562
167 NCYSRHRMELYSRPHEARSETTRPTHTYRASPARGTHRGLULEASPL 184
563 TGTGTCTCAAAAGTATGTGGCAGCTGTGATGATCTTACACCCAGCGGG 612
184 EUVALLEUYSSEIRASPRVALASERLEUASPRPHERTHPROSERCGLY 200
613 GAGTGGACATCATGCACTGCGAGCGGAGCAACGAAACCCAGACGA 662
201 GLUTRPSRPLEILEALALEUPROGLYARGARGASNGLUASPRPROASPRAS 217

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663 CTCCAGCTATGTGGACATCACCTATGACTTCATCTTGTGGCAACAC 712
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713 TCTTCTACACTATACCCATCATCCCTCGCTAGCTCATCAGCTCGCTG 762
234 EUPHERYRTHRILEASNLEULILEITLEPCYSVALLEULETHTHRSERLEU 250
763 GCCATCCGTGCTTCTACCTGCGCTCAGACTGTGATGTAAGATGACACT 812
251 ALAILEUVALRPHETRYLEUPROSERASPCYSGLYULYSMETHTHLE 267
813 TTGTATTTCTGTGCTGCTAGCACTCAGCGTGTCTGCTGCTCATCTCCA 862
267 UCYSILSEERVALLEUVALALEUTHRVALRPHLEUULEULESERL 284
863 AGATTGTGCTCCACACTCCCTCGATGTACCGCTGTTGGCAAGTACCTC 912
284 YSILEVALPROPTROTHRSEIRLEUASPRVALPROLEUVALGLYLYSTYRLEU 300
913 ATGTTTACCATGTGCTAGTACACTTCTCCATCGTACACAGCGTGTGT 962
301 MEUPHERTHMETVALLEUVALTHRPHESERILEVALTHRSEIRVALCYSA 317
963 GCTCAATGTGACACACCGCTCGCTTACACGACACCATGGCCCCGTGGG 1012
317 ILEUASNVALHISHSIARGSERPROTHRTHISHTRMETALAPROTPRV 334
1013 TCAAGGTGCTTCTCTGGAGAAAGCGCCACCGCTGCTCTTCTGTCACAG 1062
334 ALLYSVALVALRPHLEUGLULYSLEUPROTHRLEULEUPHLEUGLNGLN 350
1063 CCACGCGCACCGCTGTGCACTGACAGCTGTGCGCTTGAGAGAGCGCCAGCG 1112
351 PROARGHSIARGCYSAIARGGLNARGLEUARGLEUARGAARGGLNARG 367
1113 AGAGCGTGAAGCGGAG... GCGGTTTCTTCCGTGAAGCTTCCGCGCTG 1159
367 GGLUARGGLUGLYALGLYALALEUPHEPHEARGGLUGLYPROALALALA 384
1160 ACCCATGTACCTGCTTGTGCAACCGCTGCATGACGACGAGGCTGGCGGG 1209
384 SPRPCYSRTHCYSPHEVALASNPROALASERVALGLINGLYLEUALIGLY 400
1210 GCTTTCGAGCTGAGCCCATGACAGCGCGCGCGCTGTGTGGCGCC 1259
401 ALAPHEARGALAGLUPROTHRVALALAGLYPROGLYARGSERVALGLYPR 417
1260 ATGCAGCTGTGCGCTCCGGAAGCAGTGATGGCTGACGCTTCAATTCGCG 1309
417 OCYSSERCYSGLYLEUARGGLUVALVALASPOLYVALARGPHEILELALA 434
1310 ACCCATGCGAAGTAGATGATGATGACCGAGATGTGAGGAGAGATGAAA 1359
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1360 TACGTTGCCATGATGATGACCGCGCTTCTGTGATCTTTGTCTTGTGT 1409
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1410 CTGTGCTTGTGGAGCGTCCGATGTTCTGACGCTCTCTTCCAGAACT 1459
467 ICYSVALRPHGLYTHRVALIGLYMETRPHLEUGLNPROLEUPHEDLNASPT 484
1460 ACAGTGCACACTACTCTCTCCACCCCTGACACCTAGCTCCAGCTCCAG 1509
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seq\_documentation\_block:

ID ACHN\_HUMAN STANDARD; PRT: 502 AA.

AC p17787;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-2 CHAIN PRECURSOR.  
GN CHRN2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=90332444; PubMed=2377478;  
RA Anand R., Lindstrom J.;  
RT "Nucleotide sequence of the human nicotinic acetylcholine receptor  
beta 2 subunit gene.";  
RL Nucleic Acids Res. 18:4272-4272(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX Elliott K.J., Ellis S.B., Bereckhan K.J., Urrutia A.,  
RA Chavez-Morriga L.E., Johnson E.C., Velicelebi G., Harpold M.M.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Frontal cortex;  
RX MEDLINE=97162233; PubMed=9009220;  
RA Groot Kormelink P.J., Luyten W.H.M.L.;  
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal  
nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and  
expression of seven nAChR subunits in the human neuroblastoma cell  
line SH-SY5Y and/or IMR-32.";  
RL PNAS Lett. 400:309-314(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99373254; PubMed=10441742;  
RA Lueders K.K., Elliott R.W., Mareholz I., Mische D., Dupree M.,  
RA Hamer D.;  
RT "Genomic organization and mapping of the human and mouse neuronal  
beta2-nicotinic acetylcholine receptor genes.";  
RL Mamm. Genome 10:900-905(1999).  
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE AChR RESPONDS BY AN  
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND  
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA  
MEMBRANE.  
CC -1- SUBUNIT: NEURONAL AChR SEEMS TO BE COMPOSED OF TWO DIFFERENT  
TYPE OF SUBUNITS: ALPHA AND BETA.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL, X53179; CAA37320.1; -  
DR EMBL, U62437; AAB40115.1; -  
DR EMBL, Y08415; AAB69692.1; -  
DR EMBL, AF077186; AAD45422.1; -  
DR PIR, S10505; S10505.  
DR MIM, 118507; -  
DR InterPro: IPR001175; -  
DR InterPro: IPR002394; -  
DR Pfam: PF00065; neur\_chan. 1.  
DR PRINTS: PR00252; NRIONCHANNEL.  
DR PRINTS: PR00254; NICOTINICR.  
DR PROSITE: PS00236; NEUROTR\_ION\_CHANNEL. 1.  
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;  
KW Transmembrane; Multigene family.

FT	SIGNAL	1	25	BY SIMILARITY.
FT	CHAIN	26	502	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN.
FT	DOMAIN	26	233	BETA-2 CHAIN.
FT	TRANSMEM	234	258	EXTRACELLULAR.
FT	TRANSMEM	256	284	
FT	TRANSMEM	300	321	
FT	DOMAIN	322	458	CYTOPLASMIC.
FT	TRANSMEM	459	478	
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FT	CARBOHYD	51	51	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	168	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	485	485	N-LINKED (GLCNAC. . .) (POTENTIAL).
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alignment_scores:	Quality:	2432.00	Length:	492
Ratio:	5.087		Gaps:	2
Percent Similarity:	97.561		Percent Identity:	94.106

  

alignment\_block:  
US-07-938-154-10 x ACHN\_HUMAN ..

  

Align seg 1/1 to: ACHN\_HUMAN from: 1 to: 502

  

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90	CACAGAGAGCGGCTAGTGAGCAGCATCTTATGATCCCTCCGCTATACAA	139	CACAGAGAGCGGCTAGTGAGCAGCATCTTATGATCCCTCCGCTATACAA	139
27	pThrGluGluArgLeuValGluHisLeuLeuAspProSerArgYThrAsn	44	pThrGluGluArgLeuValGluHisLeuLeuAspProSerArgYThrAsn	44
140	AGCGATTCGTCGAGCTACTAACGCGCTGAGCTGTGATGTACACTC	189	AGCGATTCGTCGAGCTACTAACGCGCTGAGCTGTGATGTACACTC	189
44	YsLeuIleArgProAlaThrAsnGlySerGluLeuValThrValGlnLeu	60	YsLeuIleArgProAlaThrAsnGlySerGluLeuValThrValGlnLeu	60
190	ATGGATCATTTGGCTGAGCTCATTAATGTGACGAGCGGAGAGCATCAT	239	ATGGATCATTTGGCTGAGCTCATTAATGTGACGAGCGGAGAGCATCAT	239
61	MetValSerLeuAlaGlnLeuIleSerValHisGluArgGluGlnIleMe	77	MetValSerLeuAlaGlnLeuIleSerValHisGluArgGluGlnIleMe	77
240	GACCAACCATGTGCTGACACCCAGAGAGTGGAGAAATTACCGCCTCACAT	289	GACCAACCATGTGCTGACACCCAGAGAGTGGAGAAATTACCGCCTCACAT	289
77	tThrThrAsnValTrpLeuThrGlnIleTrpGluAspYrArgLeuThr	94	tThrThrAsnValTrpLeuThrGlnIleTrpGluAspYrArgLeuThr	94
290	GGAACCCCTGAGAGACTTCGACATATGAAGAAGTCCGGCTCCCTCCAAA	339	GGAACCCCTGAGAGACTTCGACATATGAAGAAGTCCGGCTCCCTCCAAA	339
94	rPlyArgProGluGlnPheAspAsnMetLysValAlaArgLeuProSerLys	110	rPlyArgProGluGlnPheAspAsnMetLysValAlaArgLeuProSerLys	110
340	CACATCTGGCTCCAGATGTGGTTCTATACAAACATGCTGACGGCATGA	389	CACATCTGGCTCCAGATGTGGTTCTATACAAACATGCTGACGGCATGA	389
111	HisIleTrpLeuProAspValValLeuTrpYrAsnAsnAlaAspGlyMet	127	HisIleTrpLeuProAspValValLeuTrpYrAsnAsnAlaAspGlyMet	127
390	CGAAGTCTCTTCTATTCCCAATGCTGTGCTCTCATGATGAGCAGCATCT	439	CGAAGTCTCTTCTATTCCCAATGCTGTGCTCTCATGATGAGCAGCATCT	439
127	rGluValSerPheTrpSerAsnAlaValAlaValSerYrAspGlySerIleP	144	rGluValSerPheTrpSerAsnAlaValAlaValSerYrAspGlySerIleP	144
440	TTTGGGCTTCACGCTGCATCTACAAAGTGATGCAAGATTAGGTGAGAG	489	TTTGGGCTTCACGCTGCATCTACAAAGTGATGCAAGATTAGGTGAGAG	489
144	hertPheuProAlaIleTrpLysSerAlaCysAlaYsIleGluValLys	160	hertPheuProAlaIleTrpLysSerAlaCysAlaYsIleGluValLys	160
490	CACCTCCATTGTGACACGACGAATTGACACATGAAGTTTGCTCATGAGC	539	CACCTCCATTGTGACACGACGAATTGACACATGAAGTTTGCTCATGAGC	539
161	HisPheProPheAspGlnGlnAsnCysTrpMetLysPheArgSerTrpTh	177	HisPheProPheAspGlnGlnAsnCysTrpMetLysPheArgSerTrpTh	177
540	CTACACACGCTACTGAGATTACCTGGTGGTCAAAAGTGATGGCCAGCTC	589	CTACACACGCTACTGAGATTACCTGGTGGTCAAAAGTGATGGCCAGCTC	589
177	rYrAspArgYrThrGluIleAspLeuValLeuLysSerGluValAlaSerL	194	rYrAspArgYrThrGluIleAspLeuValLeuLysSerGluValAlaSerL	194
590	TCGATGATCTTCACACCCAGGGGAGTGGGACATCATGCAATGCCACAGC	639	TCGATGATCTTCACACCCAGGGGAGTGGGACATCATGCAATGCCACAGC	639
194	euaSPasPheTrpProSerGlyValTrpAspIleValAlaLeuProGly	210	euaSPasPheTrpProSerGlyValTrpAspIleValAlaLeuProGly	210









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938 TCTCATGTCACAGCGTGTGTCTCAATGTCACACCGCTGCGCT 987
939 |||||||
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988 ACCGACACACCATGCGCCCTGGCTCAAGTGTCTTCTGGAGAGCT 1037
989 |||||||
305 SerThrHisThrMetProProTrpValIleValPheLeuGluArgLe 321
1038 GCCACCCCTGCTCTCTGACAGACACCGCCGCTGTGCTGACGTACG 1087
1039 |||||||
321 uProAlaTrpLeuPheMetLysAlaGProGluAsnSerProArgGlnL 338
1088 GTCTGCGCTTGAAGAGCGCCAGACAGACGCTGAGAGCGGCGGTTTC 1137
1089 |||
338 yseProAlaAsnCysLysLysThrArg..... 346
1138 TTCCTGGAAGTCTCGCTGACCCATGT.....AC 1169
1139 |||
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1170 CTGCTTTGTCACACCTGCATGATGTCAG..... 1197
1171 |||||||
362 rTyrrPheValAsnThrAlaSerAlaLysLysTrpAspMetLysIleThra 379
1198 ..GGCTTGGCTGGGCTTTCGACGCTGAGCCCATGTCAGCGCGCGGG 1245
1199 |||
379 sPThrLeuAspAsnValSerSerHisGlnAspPheArgLeuArgThrIly 395
1246 CCGCTGTGTGGGCGCATGAGCTGTGGCTCGCGGAGAGAGTGGAGGCT 1295
1247 |||
396 ThrLysPheSerPro.....GluValGlnGluAlaIleAspGlyVa 409
1296 ACCGTTTCATGCGGACACATGCGGAGTGGAGTATGATACACAGACTGGA 1345
1297 |||
409 lserPheIleAlaGlnHisMetLysSerAspAspAsnAspGlnSerValI 426
1346 GGGAGGACGTGAAATACGTTGCCATGATGATGACCGCGCTGTCTCTGG 1395
1347 |||||||
426 legLAspTrpLysTrpValAlaMetValValAspArgLeuPheLeuTrp 442
1396 ATCTTGTCTTGTCTGTCTTGTGGACCGTGGCATGTTCTCTGACCC 1445
1397 |||||||
443 lIlePheValIleuValCysValLeuGlyThrValGlyLeuPheLeuGlnPr 459
1446 TCTCTTCAGACTACACTGCGCATACC 1473
459 oleuPheGlnAsnHisIleAlaIleThr 468
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AC P19370:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-2 CHAIN (GF-BETA-2)
DE (FRAGMENT).
OS Carassius auratus (goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_Taxid=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=90384858; PubMed=2402468;
RA Hieber V.C., Bouchoy J.E., Agranoft B.W., Goldman D.;
RT "Nucleotide and deduced amino acid sequence of the goldfish neural
RT Nucleic Acids Res. 18:5307-5307(1990).";
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

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CC CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC CC MEMBRANE.
CC CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
CC CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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CC CC -----
DR EMBL: X54052; CAA37986.1; -.
DR PIR: S14703; S14703.
DR InterPro: IPR001175; -.
DR Pfam: PF00065; neur_chan. 1.
DR PROSITE: PS00236; NEUROTR_ION_CHANNEL. 1.
DR KMW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW Transmembrane; Multigene family.
FT FT NON_TER 1 1
FT DOMAIN <1 203 EXTRACELLULAR.
FT TRANSMEM 204 228
FT TRANSMEM 236 254
FT TRANSMEM 270 291
FT DOMAIN 292 421 CYTOPLASMIC.
FT TRANSMEM 422 440
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 125 139 BY SIMILARITY.
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SQ SEQUENCE 459 AA; 53040 MW; 860B1A011AA4/GF6 CRC64;

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Ratio: 4.269 Gaps: 5
Percent Similarity: 82.766 Percent Identity: 67.021

alignment_block:
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20 lAsnLysSerGlnGlnValThrIleGlyIleLysValSerLeuAlaGlnL 37
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37 euLleSerValAsnGluArgGlnIleMetThrTrpAsnValIleTrpLeu 53
259 ACCGAGAGTGGGAAGATTACCGGCTCAGATGAGAGAGCTTGAGACTTTCGA 308
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310 |||
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359 TGGTTCATACACATGCTGACGCGATGATGAGAGTCTCTCTATATCC 408
360 |||
87 lValLeuTrpAsnAsnAlaAspGlyValTrpGluValSerPheTrpCys 103
409 AATGCTGAGCTCTCTATGATGAGGAGCATGTTGGCTACACATGTCAT 458
410 |||
104 AsnAlaValIleSerAsnThrGlyAspIlePheTrpLeuProAlaIle 120

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459 CTACAGAGTCATGCAAGATTGAGGTGAGACACTTCCATTGACGAC 508
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120 eTfLysSerAlaCysAlaIleGluValArgAsnProPheAspGing 137
509 AGAATTGACCAATGAGTTGGCTCATGAGCACTACGAGTACAGATT 558
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137 LhAsnCysThrLeuLysPheArgSerThrPheThrAspArgThrLeu 153
559 GACCTGGTCTCAAAAGTAGATGCGCAGTGTGATGACTTACACCCAG 608
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154 AsPheValLeuThrSerAspPheAlaSerArgAspPheThrProse 170
609 CGGGAGTGGAGCATCATGCGACCTGCGAGCGGACCAAGCAAGACCCG 658
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187 snAspLeuThrTyrlleuAspIleThrTyAspPheValIleLysArg 203
709 CCACCTCTTACATCATCAACCTCATCATCCCTGCTACATCAGCTC 758
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204 ProLeuPheThrThrLeuAsnLeuIleIleProCysValLeuIleTh 220
759 GCTGGCATCTGGTCTTCTACCTGCTCAGACCTGTGTGTAAGAAGA 808
|||||
220 rLeuAlaIleLeuValPheTyrlleuProSerAspGlyLysValT 237
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237 hrLeuLysMetSerValLeuLeuAlaLeuThrValPheLeuLeu 253
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1109 AGCGAGAG..CGTGAAGGCGAGCGGCTTCTTCTCCGT 1143
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1144 GAAGTCTCGGCGCTGACCACTGATACCTGCTTGTCAACCCGATCA 1193
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353 AsPAspProGlyArg.. 357
1194 GCAGGCTTGGCTGGGCTTTCGAGCTGAGCCACTGACGCCGCCGG 1243
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1244 GCGGCTCTGGGCGCATGACAGTGGC.. 1272
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364 ..ValGlyAspLeuProGlyLysSerGluPheArgGlnArgVal 377
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1402 GTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1451
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444 eGlnSerTyr 447

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ID ACHP_HUMAN STANDARD; PRT; 498 AA.
AC P30926; Q16607;
DT 01-JUL-1993 (Rel. 26, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-4 CHAIN PRECURSOR.
GN CHRB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Morales L.E., Johnson E.C., Velicic G., Harpold M.M.:
RA Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
RL
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97347299; PubMed=9203638;
RA Gerzanich V., Kuryatov A., Anand R., Lindstrom J.:
RA "Orphan" alpha6 nicotinic AChR subunit can form a functional
RA heteromeric acetylcholine receptor."
RT Mol. Pharmacol. 51:320-327(1997).
RL
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.:
RA "Cloning and sequence of full-length cDNAs encoding the human neuronal
RA nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32."
RL FEBS Lett. 400:309-314(1997).
RN
RN [4]
RP SEQUENCE OF 48-498 FROM N.A.
RA MEDLINE=93050165; PubMed=1330682;
RA Tarroni P., Rubboli F., Chini B., Zwart R., Oortgiesen M., Sher E.,
RA Clementi F.:
RA "Neuronal-type nicotinic receptors in human neuroblastoma and
RT small-cell lung carcinoma cell lines."
RL FEBS Lett. 312:66-70(1992).
CC
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE AChR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL AChR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

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1  |||
416 rserglyarphearglnasprvalglnalvalauleuglyvalserp 433
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433 hellelalaInihsmelysanaasprglnasprglnaserlvalaIgu 449
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1401 TGCCTTGTCTGTCTTGGACCGCTGCATGTCCTGCAGCTCTCT 1450
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1451 TCACAGACTACACTGCACACT 1470
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ID ACHP_RAT STANDARD; PRT; 495 AA.
AC P12392; 063361;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-4 CHAIN PRECURSOR (NON-ALPHA 2) (N-ALPHA 2).
DE CHRNA4 OR ACRB4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116.
RA [1]
RP SEQUENCE FROM N.A. (SHORT FORM).
RA MEDLINE=90380390; PubMed=2642007;
RA Duvoisin R.M., Deneris E.S., Patrick J., Heinemann S.;
RT "The functional diversity of the neuronal nicotinic acetylcholine receptors is increased by a novel subunit: beta 4."
RT Neuron 3:487-496(1989).
RN [2]
RP SEQUENCE FROM N.A. (SHORT FORM).
RA MEDLINE=90170954; PubMed=1689727;
RA Boulter J., O'Shea-Greenfield A., Duvoisin R.M., Connolly J.G., Wada E., Jensen A., Gardner P.D., Ballivet M., Deneris E.S., McKinnon D., Heinemann S., Patrick J.;
RA "Alpha 3, alpha 5, and beta 4: three members of the rat neuronal nicotinic acetylcholine receptor-related gene family form a gene cluster."
RT J. Biol. Chem. 265:4472-4482(1990).
RN [3]
RP SEQUENCE FROM N.A. (LONG FORM).
RA TISSUE=Superior cervical ganglion;
RA MEDLINE=89140821; PubMed=2918319;
RA Isenberg K.E., Meyer G.E.;
RT "Cloning of a putative neuronal nicotinic acetylcholine receptor subunit."
RT J. Neurochem. 52:988-991(1989).
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OR SUBUNITS: ALPHA AND NON-ALPHA (BETA). BETA-4 SUBUNIT CAN BE COMBINED TO ALPHA-3, ALPHA-3, OR ALPHA-4 SUBUNITS TO GIVE RISE TO FUNCTIONAL RECEPTORS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM AND A SHORT FORM (SHOW HERE). ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN THE BRAIN, IT IS DETECTED IN THE MEDIAL HABENULA. IN THE PERIPHERAL NERVOUS SYSTEM, IT IS FOUND AT LEAST IN THE ADRENAL GLAND.

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CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
DR EMBL; U42976; AAA85212.1; -
DR EMBL; M33953; AAA41668.1; -
DR EMBL; J05232; AAA41668.1; JOINED.
DR EMBL; M89971; AAA41668.1; JOINED.
DR EMBL; M33951; AAA41668.1; JOINED.
DR EMBL; M89989; AAA41668.1; JOINED.
DR EMBL; M33952; AAA41668.1; JOINED.
DR EMBL; X15834; CAA33839.1; -
DR PIR; J50353; J50353.
DR PIR; B35721; B35721.
DR InterPro; IPR001175; -
DR InterPro; IPR002394; -
DR Pfam; PF00065; neur_chan.1.
DR PRINTS; PR00254; NICOTINCR.
DR PRINTS; PR00236; NEURON_ION_CHANNEL.1.
DR PROSITE; PS00236; IONIC_CHANNEL; Glycoprotein; Signal;
KW Postsynaptic membrane; Ionic channel; Glycine family; Alternative splicing.
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Alignment_scores:
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Ratio: 4.025 Gaps: 4
Percent Similarity: 82.500 Percent Identity: 63.125

Alignment_block:
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188 TCATGTATCATTCGCTACGCTCATTTAGTGTGACAGCGAGCGAGACATG 237
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57 euGlLeuSerIeuSerGlnleuIleSerValaAngIuaTgIuGlnIle 73

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338 AACCATCTGGCTCCAGATGTGTTCTATACAAATCTCAGCGCATG 387
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388 TACGAGTCTCCTTATCCAAATGCTGCTGCTCTATATGAGCAGAT 437
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638 GCCGACGACGAGAACCCAGACGACTCCACTATGTGACATCCTCAT 687
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207 LysArgArgThrValAsnProGlnAspProSerTyrValAspValTrpTyr 223
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738 CCCCTGGCTACTCATCACTCGCTGCCATCTGCTCTTCTACTCCCT 787
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938 TCTTCATCTGACACAGCGTGTGTGCTCAATGTGACACACGCTCGCT 987
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988 ACCACGACACCATGGCCCTCGTCAAGGTGTCTCTCTGTGAGAAAGCT 1037
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324 SerThrHisThrMetAlaSerTrpValLysGluCysPheLeuHisLysSle 340
1038 GCCCAACCTGCTCTTCTGACGACGACGACGCTGTGACGCTGACG 1087
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1264 AGCTGTGCGC..... 1272
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1273 .....CTCGGGGAGACAGATGATGATGCGGTACGCTTACCTGGAGCCACA 1315
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ID ACH2_CHICK STANDARD: PRT: 528 AA.
AC P09480;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, last sequence update)
DT 01-OCT-2000 (Rel. 40, last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN PRECURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88283624; Pubmed=3267226;
RA Nel P., Oneyser C., Alliod C., Couturier S., Bailivet M.;
RT "Genes expressed in the brain define three distinct neuronal
RT nicotinic acetylcholine receptors."
RL EMO J. 7:595-601(1988).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
CC FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
CC THREE NON-ALPHA CHAINS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC
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635 CAGGCCGACGACGACGAGAACCCAGACGAC.....TCCACCTATGCG 675
237 hGlyThrTyrTrpAsnSerLysTyrAspGlyCysAlaGluIleTyrPro 253
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404 LeuGluSerAsnValAspAlaGluGluValValValValValGluGlu 420
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420 uAspArgTrpAla.....CysAlaGlyHisValAlaPro...SerValG 434
1196 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
434 LyrThrLeuGlySerHisGlyHisLeuHisSerGlyValAserGlyProLys 450
1243 .....GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1271
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1322 GTGAGATGATGACCAAGATGAGAGGAGAGAGAGAGAGAGAGAGAGAG 1371
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499 ValIleAspArgIlePheLeuTrpLeuPheIleIleValCysPheLeuG 515
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515 yThrIleGlyLeuPheLeuProPro 523

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seq_documentation_block:
ID ACH4_RAT STANDARD; PRT; 630 AA.
AC P09483; Q35769;
DT 01-MAR-1989 (Rel. 10, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-4 CHAIN PRECURSOR.
CN CHNM4 OR ACRA4.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Hypothalamus, and Hippocampus;
RX MEDLINE=87159533; PubMed=3829125;
RA Goldman D., Deneris E.S., Luyten W., Kochhar A., Patrick J.,
RA Heinemann S.;
RT "Members of a nicotinic acetylcholine receptor gene family are
RT expressed in different regions of the mammalian central nervous
RT system.";
RL Cell 48:965-973(1987).
RN [2]
RP REVISIONS.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA Hartley M., Goldman D.J., Heinemann S.F.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Boulter J., Deneris E., Evans K., Heinemann S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PARTIAL SEQUENCE OF 31-47.
RX MEDLINE=87276531; PubMed=3609304;
RA Whiting P., Esch F., Shimazaki S., Lindstrom J.;
RT "Neuronal nicotinic acetylcholine receptor beta-subunit is coded for
RT by the cDNA clone alpha 4.";
RL FEBS Lett. 219:459-463(1987).
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-4 SUBUNIT CAN BE
CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA-4-1 (SHOWN HERE) AND
CC ALPHA-4-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN VARIOUS REGIONS OF THE CENTRAL NERVOUS
CC SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M15682; AAA41676.1; -
DR EMBL: L31620; AAC97071.1; -
DR EMBL: AF007212; AAB64439.1; -
DR PIR: A26456; A26456.
DR InterPro: IPR001175; -
DR PIR: A26456; A26456.
DR PIR: A26456; A26456.
DR Pfam: PF00065; neur_chan; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR PRINTS: PR00254; NICOTINICR.
DR PROSITE: PS00236; NEUROT_RON_CHANNEL; 1.

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465 LeuLeuLysAlaArgSerLeuSerValGlnHisValProSerSerClnG1 481
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481 uAlaAlaGlnAspGlyIleArgCysArgSerArgSerIleGlnTYRCysV 498
1198 .....GGCTTGCGCTGGGCTTTCGAGCTGAGCCACCTGCA... 1233
498 alSerClnAspGlyAlaIleSerLeuAlaAspSerIleProThrSerSer 514
1234 .....GCCGGCCCGGGGGCG...TCGCT 1253
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1254 GGGGGCATCGACTGTGGCTCCGGAA..... 1281
531 aserProCysLysCysThrCysLysGluProSerProValSerProValT 548
1281 ..... 1281
548 hValLeuLysAlaGlyIleThrLysAlaProProGlnHisLeuProLeu 564
1282 .....GCAGTGGATGGCGTACCGCTTCATTCGGGACCA 1313
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1314 CATCGCAAGTGAAGATGATGACACAGAGTGAGGAGAGCACTGAATAGC 1363
581 sleuLysAlaGlnAspThrAspPheSerValLysGluAspTrpLysTyrV 598
1364 TTGGCATGTGATGACGGCGCTTCCGTCGAGATCTTGCTTGCTGCTGT 1413
598 alAlaMetValIleAspArgIlePheLeuTrpMetPheIleIleValCys 614
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seq_name: Swissprot_39:ACH2_RAT
seq_documentation_block:
ID ACH2_RAT STANDARD; PRT; 511 AA.
AC P12389; 008952;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN PRECURSOR.
GN CHRNA2 OR ACR42.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=88178113; Pubmed=2832952;
RA Wada K., Ballivet M., Boulter J., Connolly J., Wada E., Denieris E.S.,
RA Swanson L.W., Heinemann S., Patrick J.;
RT "Functional expression of a new pharmacological subtype of brain
RT nicotinic acetylcholine receptor.";
RL Science 240:330-334(1988).
RN [12]
RP REVISIONS.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA Boulter J.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE
CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.

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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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CC or send an email to license@sib-sib.ch).
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DR EMBL: J10077; AAB60900.1; -
DR EMBL: M20297; AAA40664.1; -
DR EMBL: M20292; AAA40664.1; JOINED.
DR EMBL: M20293; AAA40664.1; JOINED.
DR EMBL: M20284; AAA40664.1; JOINED.
DR EMBL: M20285; AAA40664.1; JOINED.
DR EMBL: M20296; AAA40664.1; JOINED.
DR InterPro: IPR001175; -
DR InterPro: IPR002394; -
DR Pfam: PF00065; neur_chan.1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR PRINTS: PR00254; NICOTINICR.
DR POSTITE: PS00236; NEUROTR_ION_CHANNEL.1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 27
FT CHAIN 28 511
FT DOMAIN 28 241
FT TRANSMEM 242 262
FT TRANSMEM 274 292
FT TRANSMEM 308 329
FT DOMAIN 330 484
FT TRANSMEM 485 503
FT DOMAIN 381 402
FT DISULFID 160 174
FT DISULFID 224 225
FT CARBOHYD 56 56
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FT CONFLICT 494 494
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5 Hisser...AlaLeuGlnPheTrpThrHisLeuTyrLeuTrpCysLeu 20
||||| ..... |||||
64 CTGTGCTCAGCGGCTTTTG.....GCAACTGACACAGAG 97
||| ..... |||
20 uLeuValProAlaValLeuThrClnGlnGlySerHisThrHisAlaGln 37
||||| ..... |||||
98 AGCGCTTAGTGAGACATCTTAGATCCCTCCGCTATACAGCTGATT 147
||||| ..... |||||
37 spragLeuPheLysHisLeuPhe.....GlyGlyTyrAsnArgTrpAla 51
||||| ..... |||||
148 GTCGCTACTTAAGCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 197
||||| ..... |||||
52 ArgProValProAsnThrSerAspValValIleValAlaArgPheGlyLeu 68
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198 ATGGCTCAGCTCATTTAGTGTGACAGAGCGGAGCAGATCATGACACCA 247

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68 rtleaglInleuileaspyalaspGluysasnGlnmetMethrThra 85
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85 snValrpleuLysGlnGluTrpAsnSprLyLysleuArGtrpAspPro 101
298 GAGACTGTGACAAATAGAGAAGTCGGCTCCCTCCAAACACATCTG 347
102 AlagluPhelGlysnValThrSerleuArGValProSerGlnMetIleTr 118
348 GCTCCAGATGTGTTCTATACAACATGCTGAGCGCATGACAGACT 397
118 pIleProaspIleValleuLysrAsnAlaAspGlyGluPhelAlaValT 135
398 CCTTATTCATGCTGTGCTCCATATGATGACACATCTTTGGCTA 447
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448 CCACCTGCATTCACAGAGTCGATGACAGATTGAGTGAAAGCACTGCC 497
152 ProPrAlAlleLyrLysSerSerCysSerIleAspValThrPhelPhePr 168
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648 CGAGAACCCAGACGAC.....TCCACCTATGTGACATCACCTATG 688
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689 ACTTCATCATCTGTCGCAACCATCTTTCATACATAACCTATCATC 738
235 yTrheValIleArGArGLeuProLeuPheTrpIleAsnLeuIleIle 251
739 CCTGTGACTCATCACCTGCGTGGCCATCGTCTTCTACCTGCGCCTC 788
252 ProCysLeuLeuIleSerCysLeuThrValleuValPheTrpLeuPro 268
789 AGACTGTGTGAAGAAGATGACACTTGTATTTCTGTCTGTACACTCA 838
268 rGluCysGlyGluLysIleThrLeuCysIleSerValleuLeuSerLeuT 285
839 CGGTGTTCCTGGCTGCATCTCCAAAGATGTGGCTCCCACTCCCTGAT 888
285 hValrPheLeuLeuLeuIleThrGlnIleLeuProSerTrpSerLeuVal 301
889 GTACCGCTGTGGCAAGTACTCATGTTTACCATGGGAGTACACCTT 938
302 IleProLeuIleGlyGluTrpLeuLeuPheThrMetIlePheValThrIle 318
939 CTCATCTGTACACAGCGTGTGTCTCAATGTGACACACCGCTGCGCTA 988
318 uSerIleValIleThrValPheValleuAsnValHlsHlsrGserPros 335
989 CACGAGACACCATGAGCCCTGGTCAAGTGTCTTCTGTGAGAAGCTG 1038
335 eTrhrHlsAsnMetProAsnTrpAlaArGValAlaLeuLeuGlyArGVal 351
1039 CCCACCCCTGCTTCTCTGACAGAG..... 1062
352 ProArGTrpLeuMetMetAsnArGProLeuProProMetGluLeuHlsG 368
1063 .....CCACGCCACCGCTGTGTGACAGCTGACCGCTC 1090

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368 ySerProAspLeuLysLeuSerProSerTrpHlsTrpLeuGluThrAsnM 385
1091 TGGCGTTGAGAGGGCGCCAGCGAGAGCTGAGGGCAGGGGTTTCTTC 1140
385 eAspAlaGlyGluArGValGlnGluTrpGlnGluGlu..... 397
1141 CGTGAAGTCTTCGCGCTGACCCATCTACTGCTTGTCTCAACCTGCATC 1190
398 ...GluGlnGluAspGluAsnIleCysValCysAlaGlyLeuProAspSe 413
1191 AGTCAGGGCTTGCTGGGCT.....TTCGAGCT...G 1222
413 rSerMetGlyValleuLyrGlyHlsGlyGlyLeuHlsleuArGAlaMetG 430
1223 AGCCCACTGACAGCGGCCCGGGGGCGCT.....GTGGGCCA 1260
430 LuProGluThrLysTrpThrProSerGlnAlaSerGluIleLeuLeuSerPro 446
1261 TGCAGCTGTGGCTCCGGAGACAGTGAATGGCGTTCATTTGCGGA 1310
447 .....GlnIleGlnAlaLeuGlnGlyValHlsTrpIleAlaAs 460
1311 CCACATGCAAGTAGAGATGATGACCAAGCTGTGAGGAGAGCTGAAT 1360
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seq.name: SwissProt_39:ACH4_HUMAN
seq_documentation_block:
ID ACH4_HUMAN STANDARD; PRT; 627 AA.
AC P43681;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-4 CHAIN PRECURSOR.
GN CHRNA4 OR NACRA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95237608; PubMed=7721089;
RA Monteggia L.M., Gopalakrishnan M., Touma E., Idler K.B., Nash N.,
RA Arneric S.P., Sullivan J.P., Giordano T.;
RT "Cloning and transient expression of genes encoding the human alpha-4
RT and beta-2 neuronal nicotinic acetylcholine receptor (nAChR)
RT subunits.";
RL Gene 155:189-193(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96430009; PubMed=8833159;
RA Steinlein O.K., Welland S., Stood J., Propping P.;
RT "Exon-intron structure of the human neuronal nicotinic acetylcholine
RT receptor alpha 4 subunit (CHRNA4).";
RL Genomics 32:289-294(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelli G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional

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220 hrrgylstyrglucysCysAlaGluIleTyrProAspIleThrVal 236
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237 PheValIleThrArgLeuProLeuPheTyrThrIleAsnLeuIleLeu 253
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253 cGlyLeuLeuIleSerCysLeuThrValLeuValPheTyrLeuProSerG 270
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387 GluProGluGluGluProAlaThrSerGlyThrGlnSerLeuHisPr 403
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1109 AGCGAGAGCGCTGAGGAGCGCGTTTCTCGTGAAGT..... 1149
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470 isMetSerSerProGlyGluAlaVal.....GluGlyGlyValArg 483
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1152 TGGCGCGGAC..... 1161
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1224 GCCCAGTACAGCGCGCGCGCTGTGTGGGCCATGACATGCTGTGGCC 1273
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597 lIleAspArgIlePheLeuTyrMetPheIleIleValCysLeuGluGlyT 614
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ID ACH4_CHICK STANDARD; PRT; 622 AA.
AC P09482;
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-4 CHAIN PRECURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88283624; PubMed=3267226;
RA Neff P., Oneyser C., Alliod C., Couturier S., Bailivet M.;
RT "Genes expressed in the brain define three distinct neuronal
RT nicotinic acetylcholine receptors."
RL EMBL J. 7:595-601(1988).
RN [2]
RP MYOGENESIS OF GLU-289, AND SUBUNITS.
RX MEDLINE=91172320; PubMed=2005979;
RA Cooper E., Couturier S., Bailivet M.;
RT "Pentameric structure and subunit stoichiometry of a neuronal
RT nicotinic acetylcholine receptor."
RL Nature 350:235-238(1991).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
CC FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
CC THREE NON-ALPHA CHAINS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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1197 GGGCTTGGCTGGGCTTCCAGAGTGAAGCC..... 1227
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424 rgllylnlntsermetleuhlsproglupropoglnvalthrlyssers 441
1228 ..... ACTGACGCC 1236
441 erprrlyprosercysylsProleuseratprhrcInlthrlyserlle 457
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458 SerlysglyArGserleuSerValGlnGlnMetlySerProAsnlysnh 474
1257 ..... 1257
474 rglulglulyserrlleArGysarGseratGserlleGlnlyCyslytl 491
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1258 ....CSATGCACTGT..... 1269
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1320 AAGTAGAGATGATGACAGAGATGTGAGGAGAGACTGGAATACGTGGCA 1369
574 gAlaGlnAspAlaAspSerValLysGlnAspTyrLysTylValAlaIam 591
1370 TGGTAGTGGAGCGCTGTGCTGTGATGATCTTGTCTTGTCTGTGCTTT 1419
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608 GlyThrValGlyleuPheleuProPro 616

seq_name: SwissProt_39:ACH3_CARAV
seq_documentation_block:
ID ACH3_CARAV STANDARD: PRT: 512 AA.
AC P18845:
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-
DE ALPHA-3).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=90384844; PubMed=2402459;
RA Hieber V.C., Bouchey J.E., Agratoff B.W., Goldman D.;
RT "Nucleotide and deduced amino acid sequence of the goldfish neural
RT nicotinic acetylcholine receptor alpha-3 subunit.";
RL Nucleic Acids Res. 18:5293-5295(1990).
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

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CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X54051; CAA37985.1; -.
DR PIR: S11230;
DR InterPro: IPR001175; -.
DR InterPro: IPR002394; -.
DR Pfam: PF00065; neur_chan.1.
DR PRINTS: PR00254; NRIONCHANNEL.
DR PRINTS: PR00254; NICOTINICR.
DR PROSITE: PS00236; NEURONR_ION_CHANNEL.1.
KW Receptor; Postsynaptic membrane; Ionic channel; glycoprotein; signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 ? 512
FT CHAIN ? 512
FT DOMAIN ? 232
FT TRANSMEM 233 257
FT TRANSMEM 265 283
FT TRANSMEM 299 320
FT DOMAIN 321 485
FT TRANSMEM 486 505
FT DISULFID 151 165
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FT CARBOHYD 47 47
FT CARBOHYD 164 164
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4 AlaSerArgIleThrIlePheleuThrValleuIleHlsGlnI 20
75 GGTTTGGGAACAGACACAGAGAGCGGCTAGTGAGCATCTTAGATC 124
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20 ucylserSerlysglyGlnAspArgleuPheArGylsleuPhe... 35
125 COTCCCGGTATACAGCTGATTCGTCACGCTACTAAGCGCTGAGCTG 174
|||||
36 ..ArgArgTyrAsnGlnIlePheArgProValGlnAsnValSerAspPro 51
175 GNGACTGACAGCTCATGATATGATGCGTACGCTGATGATGATGATGACGA 224
|||||
52 ValThrValGlnPheGlnValSerIleSerGlnIleValValAspG1 68
225 GCGGAGAGATCATGACACCAATGTCGTGCGTGAACCCAGAGCTGGAG 274
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68 wValAsnGlnIleMetGlyThrAsnLeuThrPheArGhlsIleTyrAsnA 85
275 ATTACCGGCTCATGAGAGCGTGAAGACTTCGACCAATATGAAGAAAGTC 324

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448 nasngluAlaLysGluIleGlnaspaspTrpLysTyValAlaMetValI 465  
1376 TCGACCGCCTGTCTGTGATCTTGTCTTGTGCTGTGCTTGGACC 1425  
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465 leaspargilepheleutrpValpheileleuValCysileuGlyThr 481  
1426 GTGGCATGTCTCGACGCTTC 1449  
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482 AlaGlyLeupheleuGlnProleu 489

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1307 CGGACACATGCGAAGTAGGATGATGATGACCGAAGTGTGAGGGAGGACTGG 1356
1337 |||||||
1344 IAApRHisMeIdArgSerGlnuSprAspArgGlnSerValArgGluuSpr 450
1357 AAATAGCTTGCCATGTGATGATGCAGCCGCTGTCTCTGTGGATCTTGTCTT 1406
1407 |||||||
1451 LysTyRValAlaMetValIleAspArgLeuPheLeuTrpIlePheValpH 467
1407 TGCTGTGCTCTTTGGAGCCGCGGCGATGCTCTGCAGCCTCTCTTCGAGA 1456
1467 |||||||
1467 eValCysValPheGlyThrIleGlyMetPheLeuIdnProLeuPheGlnA 484
1457 ACTAGACTGCCACCTACCTCTCCCTGCACCCCTGCACACTGCAGTCCAGCTCC 1506
1484 snTyRThrAlaThrThrPheLeuHisSerAspHisSerAlaProSerSer 500
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111
501 Lys 501
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AC Q9R291;
DT 01-MAY-2000 (TREMBLrel, 13, Created)
DT 01-MAY-2000 (TREMBLrel, 13, last sequence update)
DT 01-MAY-2001 (TREMBLrel, 16, last annotation update)
DE NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR BETA 2 SUBUNIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Schuetz U.;
RT "Cloning of the beta 2 subunit of the mouse neuronal nicotinic
RT acetylcholine receptor.";
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL: AF145286; AAD33069.1; -.
DR InterPro: IPR001175; -.
DR Pfam: PF00065; neur_chan; 1.
DR PRINTS: PR00252; NR10NCCHANNEL.
DR PROSITE: PS00236; NEURON_ION_CHANNEL, 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 501 AA; 57127 MW; 1BB268290F2AA9F4 CRC64;
Alignment_scores:
Quality: 2540.00 Length: 501
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Alignment_block:
US-07-938-154-10 x Q9R291 ..
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60 TTGGCTGTGCTCAGGGGTTTGGGAAGTACACAGAGAGACCGGCTGAGTG 109
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17 uTPreucysSerGlyValIleuGlyThrValIhrgIuGluArgLeuValG 34
||||| |||||||
110 AGCATCTCTAGATCCCTCCGCTATACAGAGTGATTGTCACAGCTACT 159
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34 IuHIsleuLeuAspProSerArgTyRAsnIlyLeuIleArgProAlaThr 50
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160 AAGGCTCTGAGTGGTACTGATACAGCTCATGGTATCATTTGGCTAGCT 209
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    51 AsndlyserGluLeuValThrValGlnLeuMetValSerLeuAlaGlnLe 67
210 CATTAGTGTACAGAGCGGAGAGATCATACACCAATGTCTGGCTGA 259
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    67 uileserValHisGlnArgGlnGlnIleMetThrThrAsnValIrrpLeut 84
260 CCCAGAGTGGAGAGATTACCGCTCATATGAAAGCCTGAGAGACTTGAC 309
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    84 hrcngluTrpGluAspTyrArgLeuThrTrpLysProGluAspPheasp 100
310 AATATGAGAAAGCGGCGCCCTTCAACACATCTGGCTCCCGAGATGT 359
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    101 AsnMetLysLysValArgLeuProSerLysHisLileTrpLeuProAspVa 117
360 GGTTCATACACAAATGCTACGCGCATGTACGAAGTCTCTTATTTCCA 409
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    117 lValLeuTyrAsnAsnAlaSpGlyMetTyrGluValSerPheTyrSera 134
410 ATGCTGTGCTCTCTATGATGAGCAGATCTTTGGCTACACCTGCCATC 459
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    134 snAlaValAlaSerTyrAspGlySerIlePheTrpLeuProAlaIle 150
460 TACAGAGTGCATGACAGATTGAGTGAGACCTTCCATTGACCGACA 509
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    151 TyrLysSerAlaCysLysIleGluValLysHisPheProPheAspGlnG 167
510 GAATTGCACCATGAAGTTGCTCATGAGACCTTACGACCGTACTGAGATTG 559
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    167 nasrCysThrMetLysPheArgSerTrpThrTyrAspArgThrGluIleA 184
560 ACCTGGTGCTCAAAAGTGAATGGCCAGCTGATGACTTACACCCAGC 609
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    184 spleuValLeuLysSerAspValAlaSerLeuAspPheThrProser 200
610 GGGGAGGGGACATCATGCGACCTGCCAGGCGAGCGAGAGAAACCCGGA 659
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    201 GlyIuTrpAspIleIleAlaLeuProGlyArgAsnGlnAsnProAs 217
660 CGACTCCACCTATGTGACATCACCTATGACTTATTCATTCGTGCGCAAC 709
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    217 pAspSerThrTyrValAspIleThrTyrAspPheIleIleArgArgLysP 234
710 CACTCTTCTACACTATACACTCATCATCCCTGCTACTCATACCTCG 759
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860 CCAAGATTGTGCTGCCACCTCCCTCGATGTAACCGCTGTGGGCAAGTAC 909
    |||||||
    284 erLysIleValProProThrSerLeuAspValProLeuValGlyLysTyr 300
910 CTCATGTTTACCATGGTCTGTGCTACCTTCCATCGACACAGGCTGG 959
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    301 LeuMetPheThrMetValLeuValThrPheSerIleValThrSerValCys 317
960 TGTGCTCATATGTGACACACCGCTCCGCTTACACGACACCATGAGCCCT 1009
    |||||||
    317 sValLeuAsnValHisHisArgSerProThrThrHisThrMetAlaProT 334
1010 GGGTAAAGTGGTCTTCTGGAGAAAGCTGCCACCTGTCTTCTGCGAG 1059
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1110 GCGAGAGCGTGAGGCGAG...GCGGTTTTTCTCCGTGAAGGCTCTGCGG 1156
    |||||||
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1157 CTGACCCATGACCGCTTGTGTCAACCTGCATCATGACACAGGCTGTGCT 1206
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seq_documentation_block:
ID 09ROC3 PRELIMINARY; PRT; 500 AA.
AC 09ROC3;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR BETA 2 (FRAGMENT).
GN ACRB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=99373254; PubMed=10441742;
RA Lueders K.K., Elliott R.W., Marenholz I., Mischke D., Dupree M.,
RA Hamer D.;
RT "Genomic organization and mapping of the human and mouse neuronal
RT beta2-nicotinic acetylcholine receptor genes.";
RL Mamm. Genome 10:900-905(1999).
CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL: AF077187; AADA4476.2; -.
DR InterPro: IPR001175; -.
DR Pfam: PF00065; neur_chan. 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR PROSITE: PS00236; NEUROTR_ION_CHANNEL. 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
FT NON_TER 500 500

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50 SEQUENCE 500 AA: 57070 MM; FBE8382F78C5D766 CRC64;

alignment\_scores:

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Ratio: 5.120 Gaps: 3  
Percent Similarity: 98.004 Percent Identity: 96.008

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US-07-938-154-10 x Q9ROC3 ..

Align seg 1/1 to: Q9ROC3 from: 1 to: 500

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17 utrLeuCysSerGlyValLeuGlyThrAspThrGluGluArgLeuValG 34
110 AGCATCTCTTAGATCCCTCCGCTATACAGAGCTGATGTCCTCCAGCTACT 159
34 LuHsLeuLeuAspProSerAlaGlyAsnLysLeuLeuLeuProAlaThr 50
160 AACGCGCTGAGCTGTGCTGACTGTACAGCTCATGATGATTCATTGGCTCAGCT 209
51 AsnGlySerGluLeuValThrValGlnLeuMetValSerLeuValGlnLeu 67
210 CATTTGTTGCGACGAGCGGAGGAGATCATGATGACACCAATGTTGGCTGTA 259
67 uHsSerValHsGluArgGluGlnLeuLeuMetThrThrAsnValThrLeu 84
260 CCCAGAGCTGGGAGATTACCGCTCACATGGAAGCTGAGAGCTGAGCTCGAC 309
84 hrGlnGluTrpGluAspGlyArgLeuThrTrpLysProGluAspPheAsp 100
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101 AsnMetLysLysValArgLeuProSerLysHisIleTrpLeuProAsp 117
360 GGTCTTATACAAACATGCTGAGCGGATGAGAGTCCCTCTTATTTCA 409
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460 TACAAGAGTGCATGCAGATGAGGTGAAGCACTTCCCTTTGACCAGCA 509
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167 nasCysThrMetLysPheArgSerTrpThrTrpAspArgThrGluIle 184
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184 spleuValLeuLysSerAspValAlaSerLeuAspAspPheThrProser 200
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217 pasPserThrTrpValAspIleThrTrpAspPheIleIleArgGlySP 234
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234 robeuPheTrpThrIleAsnLeuIleIleProCysValLeuIleThrSer 250

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267 rLeuCysIleSerValLeuLeuAlaLeuThrValPheLeuLeuIle 284
860 CCAAGATTGTGCTCCACCTCCCTCGATGATACCGCTGTGGGCAATGAC 909
284 erLysIleValProProThrSerLeuAspValProLeuValGlyLysTr 300
910 CTCATGTTTACATGATGTGCTAGTCACTTCCATCTGATGATGACAGCTGTG 959
301 LeuMetPhe***MetValLeuValThrPheSerIleValThrSerValCy 317
960 TGTGCTCAATGTGCACACACCGCTCCCTACACGACACACATGAGCCCT 1009
317 sValLeuAsnValHsHisArgSerProThrThrHisThrMetAlaProT 334
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334 rpValLysValValPheLeuGluLysLeuProThrLeuLeuPheLeuGln 350
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1110 GCGAGAGCGTGAGGCGGAG...GCGGTTTCTTCCGTGAAGTCCGTGCGG 1156
367 narGluArgGluGluGlyAlaGlyThrLeu***PheArgGluGlyProAla 384
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401 GlyAlaPheGlnAlaGluProAlaAlaIleAlaGlyLeuGlyArgSerMetC 417
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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE CHRM82 PROTEIN.

GN CHRN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9918870; PubMed=9921897;  
 RA Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.;  
 FT "The structures of the human neuronal nicotinic acetylcholine receptor  
 beta2- and alpha3-subunit genes (CHRN2 and CHRNA3).";  
 RL Hum. Genet. 103:645-653(1998)  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
 DR EMBL: AJ001935; CAA05108.1; -.  
 DR EMBL: AJ001936; CAA05108.1; JOINED.  
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 DR EMBL: AJ001939; CAA05108.1; JOINED.  
 DR InterPro: IPR001175; -.  
 DR Pfam: PF00065; neur\_chan; 1.  
 DR PRINTS: PR00252; NRIONCHANNEL.  
 DR PROSITE: PS00236; NEUROTR\_ION\_CHANNEL; 1.  
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.  
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alignment\_block:  
 US-07-938-154-10 x Q9UEH9

Align seg 1/1 to: Q9UEH9 from: 1 to: 504

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90 CACAGAGAGGCGCTAGTGAGAGCATCTTGTAGTCCCTCCGCTATACA 139
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27 PTHGluGluArgLeuValGluHisLeuLeuAspProSerArgTyrAsnL 44
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44 yslLeuIleArgProAlaThrAsnGlySerGluLeuValThrValGlnLeu 60
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190 ATGCTATATGTCGCTACGCTCATTTAGTGTGCACGCGGAGACAGATCAT 239
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61 MetValSerLeuAlaGlnLeuIleSerValHisGluArgGluGlnIleLe 77
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240 GACCCACGATGCTGCTGACCCAGAGAGTGAGGAGATTACCGCTCACAT 289
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77 LThrThrAsnValITrPleuThrGlnGluITrProlAspTyrArgLeuThr 94
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690 CTTCATCATTTGCTGCACAACACACTTCTTACACTATCAACTCATCATCC 739
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
227 pPheIleIleArgArgLysProLeuPheTyrThrIleAsnLeuIleIleP 244
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
740 CCTGCGTACATCATGACCTCGCTGGCCATCTGCTTACCTGCGCCCTCA 789
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 rCysValLeuIleThrSerIleAlaIleLeuValPheTyrLeuProSer 260
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
790 GACTGTGCTGAAAAGATGACACTTTGTATTCTGTGTGCTTACGACTGAC 839
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
261 AspCysGlyGluLysMetThrLeuCysIleSerValLeuLeuAlaLeuTh 277
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
840 GGTGTCTCTGCTCATCTCCAGATGTGTGCTTCCGCACTCCCTCCGAG 889
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
277 rValPheLeuLeuLeuIleSerLysIleValrProProThrSerLeuAspV 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
890 TAACGCTGTGGGCAAGTACCTCATGTTTACCATGCTGTACTGACCTTC 939
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
294 alProLeuValGlyLysTyrLeuMetPheThrMetValLeuValThrPhe 310
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
940 TCCATCTGTCACAGCGGTGTGTGCTCAATGTGCAACACCGCTCCGCTAC 989
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
311 SerIleValIThrSerValCysValLeuAsnValHisHisArgSerProTh 327
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
990 CACGCAACACATGCGCCCTGGTGCAAGGTGCTTCTCGGAGAGATGTC 1039
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
327 rThrIsthrMetAlaProITrPValLysValAlrPheLeuGluLysLeuP 344
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1040 CCACGCTGCTTCTCTGACGACGACCCACGCGCTGTGCTGACGCTGACGCT 1089
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
344 rAlaIleLeuLeuPheMetGlnGlnProArgHisIleCysAlaArgGlnArg 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1090 CTGCGCTTGAGAGGCGCCAGCGAGACGCTGAGGCGAG...GCGGTTTT 1136
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
361 LeuArgLeuAlaArgArgGlnArgGlnArgGlnGluGluAlaIleLeuP 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1137 CTTCGCTGAAGTCCCGCGCTGACCCCATGATGACCTTGTTCACACCTG 1186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
377 ePheArgGlnAlaProGlyAlaAspSerCysThrCysPheValAsnArgA 394
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1187 CATCACTGACAGCGCTTGCTGGGGCTTTCGAGCTGAGCCCAT...GCA 1233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
394 lAserValGlnGlyLeuAlaGlyAlaPheGlyAlaGluProAlaProVal 410
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1234 GCGGCGCCGGGGGCGCTGTGTGGGGCCATGACGCTGTGGCTCCGGGAGAC 1283
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
411 AlaGlyProGlyArgSerGlyGluProCysGlyCysGlyLeuArgAlaAl 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1284 AGTGATGAGGCTACGCTCATTTGCGAGACCAATGCAAGAGAGATGATG 1333
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
427 aValAspGlyValAlaArgPheIleAlaAspHisMetArgSerGluAspAs 444
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1334 ACCGAGCTGTGAG...GAGCACTGCAATACGTTGCCATGGTGATC 1377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
444 spGlnSerValArgValSerGluAspTrpLysTyrValAlaMetValIle 460
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1378 GACCGCCTGTCTCTGAGATCTTGTCTTGTGCTGCTTGGAGACGT 1427

```

```

|||||
461 AsparglyleuPheLeuTrpIlePheValPheValCysValPheGlyThr11 477
1478 CGGCATGTTCCTCCGACGCGCTCTCCAGACATACAGTACGCTGACCTTCC 1477
477 eGlyMetPheLeuGlnProLeuPheGlnAsnTrpTrpThrThrPheL 494
1478 TCCACCCCTGACACCTACGCTCCAGCTCCAG 1509
494 euHisSerAspHisSerAlaProSerSerLys 504
seq_name: sp_rodent:Q9RJU5

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seq_documentation_block:
ID Q9RJU5 PRELIMINARY; PRT; 279 AA.
AC Q9RJU5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR BETA 2 (FRAGMENT).
GN ACRB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A.
RX MEDLINE=99373254; Pubmed=10441742;
RA Lueders K.K., Elliott R.W., Marenholz I., Mischke D., Dupree M.,
RA Hamer D.;
RT "Genomic organization and mapping of the human and mouse neuronal
RT beta2-nicotinic acetylcholine receptor genes.";
RL Mamm. Genome 10:900-905(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL: AF089739; AAD4504.1; -.
DR InterPro: IPR001175; -.
DR Pfam: PF00065; neur_chan; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
FT NON_TER 1
FT TER 279
SQ SEQUENCE 279 AA; 32248 MW; 6538200C9BC5D302 CRC64;

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alignment_scores:
Quality: 1452.00 Length: 279
Ratio: 5.242 Gaps: 0
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alignment_block:
us-07-938-154-10 x Q9RJU5

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Align seg 1/1 to: Q9RJU5 from: 1 to: 279

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1 GlnGluArgLeuValGlnHisLeuAspProSerArgTyrAsnLys 17
144 GATTGCTCAGCTACTACGCGCTGAGCTGAGTACTGACTGATGAGCTATG 193
|||||
17 uLeuArgProAlaTrpAsnGlySerGlnLeuValThrValGlnLeuMetV 34
194 TATCATTTGGCTACCTCATCTAGTGTGACAGACGGGAGCAGATCATGACC 243
|||||
34 alSerLeuAlaGlnLeuIleSerValHisGluArgGlnIleLeuMetTr 50
244 ACCATGTCTGCTGACCCAGAGAGTGGGAAGTATACCGCTCATATGGA 293
|||||
51 ThrAsnValTrpLeuThrGlnGlnIleTrpGlnAspTyrArgLeuThrTrpL 67

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294 GCGTAGAGACTTCGACATATGAGAAGAATCGCGCTCCCTCCAAACAGA 343
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67 sProGluAspPheAspAsnMetArgLysValAlaArgLeuProSerLysHis11 84
344 TCTGCGTCCGACATGTGCTTATATACAAATGCTGACGGCATGTACGA 393
|||||
84 lTrpLeuProAspValValLeuTyrAsnAsnAlaAspGlyMetTyrGln 100
394 GTCTCCTTATATCCAAATGCTGCGTCTCCATATGATGACGACATCTTTG 443
|||||
101 ValSerPheTyrSerAsnAlaValAlaSerTyrAspGlySerIlePheTr 117
444 GCTACCACTGCGCATCTACAAGATGATGACAAAGTATGAGTGAACACT 493
|||||
117 lPheProProAlaIleCysLysSerAlaCysLysIleGlnValLysHisP 134
494 TCCCATTTGACCGACGAGTATGACCATGATGAGTTTGCATGACGACTAC 543
|||||
134 heProPheAspGlnGlnAsnCysThrMetLysPheArgSerTrpTrpTyr 150
544 GACCGTACTGAGATTGACCTGCTGCTCAAAAGTATGAGTGGCCAGTCTGA 593
|||||
151 AspArgThrGlnLeuAspLeuValLeuLysSerAspValAlaSerLeuAs 167
594 TGACCTACACCCAGCGGAGTGGGACATGCAGCATGCGCAGTCCAGCGGAC 643
|||||
167 pAspPheTrpProSerGlyLysTrpAspIleIleAlaLeuProGlyArgA 184
644 GCACAGAGACCCAGACAGCATCCACCTATGTGACATCACTATGACTTC 693
|||||
184 rGAsnGlnAsnProAspAspSerThrTyrValAspIleThrTyrAspPhe 200
694 ATCATGTCGCAACACTCTTCTACTATACATCAACCTCATATGCCCGG 743
|||||
201 lIleIleArgArgLysProLeuPheTyrThrAsnLeuIleLeuProCy 217
744 CGTACTATACACCTCGCTGCGCATCTGCTGCTTCTACTGCGCTCAGACT 793
|||||
217 sValLeuIleThrSerLeuAlaIleLeuValPheTyrLeuProSerAspC 224
794 GTGCTGAAAAGATGACACTTTGTATTTCTGTGCTGCTAGCAGCAGGCT 843
|||||
234 ySelGlyLysMetThrLeuCysIleSerValLeuLeuAlaLeuThrVal 250
844 TTCCTGCTGCTCATCTCAAGATTGTGCTCCACCTCCCTCGATGATACC 893
|||||
251 PheLeuLeuLeuIleSerLysIleValProProThrSerLeuAspValPr 267
894 GCTGGTGGCAGTACCTCATGTTTACCATGGTGTCTA 930
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267 oLeuValGlyLysTyrLeuMetPheThrMetValLeu 279
seq_name: sp_human:Q9HQA3
seq_documentation_block:
ID Q9HQA3 PRELIMINARY; PRT; 529 AA.
AC Q9HQA3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA2 SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Rosenthal A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF311103; AAG23253.1; -.
KW Receptor.
SQ SEQUENCE 529 AA; 59765 MW; EA7062A11458BCC CRC64;

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## alignment\_scores:

Quality: 1221.00 Length: 475  
 Ratio: 3.430 Caps: 8  
 Percent Similarity: 74.947 Percent Identity: 51.789

## alignment\_block:

US-07-938-154-10 x Q9HAQ3 ..

Align seg 1/1 to: Q9HAQ3 from: 1 to: 529

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85 ACTGACACAGAGAGCGGCTAGTGGAGCATCTCTTGATCCCTCCGCTA 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 ThrGluThrGluAspArgLeuPheUlySHisLeuPhe.....ArgGlyTyr 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
135 TTACACGCTGATTCGTCAGCTCTCAAGGCTGTGAGCTGTGACTGTAC 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 rAsnArgTrpAlaArgProValArgProAsnTrpSerAspValAlaIleVal 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 AGCTCATGTATCATTTGGCTCAGCTCATTAAGTGTGCACGAGCGGAGCAG 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 rphGlyLeuSerIleAlaGlnLeuIleAspValAspGluLysAsnGln 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
235 ATCATGACCCCAATGTCTGTGACCCAGAGAGTGGAGATTAACCGCT 284
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
104 MetMetThrThrAsnValTrpLeuLysGlnGluTrpSerAspTyrLysLe 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
285 CACATGGAGCCTGAGGACTTTCGACATATGAAGAAGTCCGCGCTCCCT 334
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 uArgTrpAsnProThrAspPheGlyAsnIleThrSerLeuArgValProS 137
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
335 CCAACACATCTGGCTCCAGATGTGTCTATACAACATGTGCAGGC 384
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
137 erGluMetIleTrpIleProAspIleValLeuTyrAsnAsnAlaAspGly 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
385 ATGTACAGAACTCCCTCTATTCACATGCTGTGTCTCCATATGATGGCAG 434
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 GluPheAlaValThrHisMetThrLysAlaHisLeuPheSerThrGlyThr 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
435 CACTCTTTGGCTACACCTGCCATCTACAGAGAGTGCAGATGCAAGTTGAGG 484
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
170 rValHisTrpValProProAlaIleTyrLysSerSerCysSerIleAspV 187
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
485 TGAAGCACTTCCATTTGACGACGAGAATTCACACATGAACTTCGCTCA 534
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
187 alThrPhePheProPheAspGlnGlnAsnCysLysMetLysPheGlySer 203
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
535 TGGACCTACAGCGCTACTGAGATTGACCTGTGTGCTCAAAAGTGAATGGGC 584
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 TrpThrTyrAspLysAlaLysIleAspLeuGluGlnMetGluGlnThrVa 220
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
585 CAGTCTGTGACTTTCACACCCAGCGGGAGTGGACATCATCGACATGCG 634
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
220 lAspLeuLysAspTyrTrpGluSerGlyGluTrpAlaIleValAsnAlaT 237
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
635 CAGGCCGACGACGACGACGACGACGACGACGACGACGACGACGACG 675
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
237 hrGlyThrTyrAsnSerLysTyrAspCysLysAlaGluIleTyrPro 253
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
676 GACATCACCATTGATCATCTGATTCGTGCAAAACCATCTTCTACATAT 725
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 AspValThrTyrAlaPheValIleThrArgLeuProLeuPheTyrThrI 270
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
726 CAACCTCATCATCCCTGCTACTCATCATCTGCTGGCATCTGCTGCT 775
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
270 eAsnLeuIleIleProCysLeuLeuIleSerCysLeuThrValIleValP 287
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
776 TCTACTGCGCTCAGACGTGTGTGAAGAAGTGAAGTGAAGTGAAGTGA 825
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 heTyrLeuProSerAspCysGlyGluLysIleThrLeuCysLieserVal 303
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
826 CTGTAGACACTCACGTTCTCTGCTGCTCATCTCCAAAGATTGTGCTCC 875

```

```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 LeuLeuSerLeuThrValPheLeuLeuLeuIleThrGluIleIleProse 320
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
876 CACCTCCCTCGATGATCACCCTGCTGGGCAAGTACCCATCTTACCATG 925
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
320 rThrSerLeuValIleProIleGluGlyTyrLeuLeuPheThrMetI 337
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
926 TGGTAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
337 lPheValThrLeuSerIleValIleThrValPheValIleAsnValHis 353
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
976 CACCGCTGCTTACACGACGACGACGACGACGACGACGACGACGACG 1025
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
354 HisArgSerProSerThrHisThrMetProHisTrpValArgGlyAlaLe 370
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1026 CCTGGAGAACTGCCACCCCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 1068
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
370 uLeuGlyCysValProArgTrpLeuLeuMetAsnArgProProPro 387
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1069 ..CACCGCTGCGACGTCAGCGCTGCGC..... 1095
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387 alGluLeuCysHisProLeuArgLeuLysLeuSerProSerTyrHisTrp 403
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
404 LeuGluSerAsnValAspAlaGluGluValArgGluValAlaGluGlu 420
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1146 AGCTCTGCGGCTCACCATGATCTGCTTGTGCACCCCTGCATCAGTGC 1195
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420 uAspArgTrpAla.....CysAlaGlyHisValAlaPro...SerValG 434
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1196 AGGCTGTGCTGCGGCTTTCGAGCTGAGCCGCTGAGCCGCGCGCG... 1242
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
434 LyrThrLeuCysSerHisGlyHisLeuHisSerGlyAlaSerGlyProLys 450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1243 .....GGCGGCTGTGTGGGCGCATGCAGCTGTGG 1271
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451 AlaGluAlaLeuLeuGluGlnGluGlyLeuLeu.....LeuSerProH 465
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1272 CCTCCGGGAGACGACGAGGTGGGCTAGCGCTCATCTGCGGACCATGCGAA 1321
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
465 SmetIleLysAlaLeuGluGlnGlyValHisTyrIleAlaAspHisLeuAla 482
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1322 GTGAGATGATGACGACGAGTGTGAGGAGGAGCATGGAATACGTTGCCATG 1371
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
482 erGluAspAlaAspSerSerValLysGluAspTrpLysTyrValAlaMet 498
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1372 GTGATGACCGGCTGTCTGCTGATCTTGTCTTGTCTGTCTGTCTTGG 1421
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
499 ValIleAspArgIlePheLeuTrpLeuPheIleIleValCysPheLeu 515
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1422 GACCGTGGCATGTTCTGTCGACGCT 1446
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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seq_documentation_block:
ID Q9ET51 PRELIMINARY; PRT; 629 AA.
AC Q9ET51;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 4 SUBUNIT.
GN ACRA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LONG SLEEP SELECTED LINE;
RA Stitzel J.A., Jimenez M., Smolen A., Modir J.;

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"Cloning of mouse nicotinic acetylcholine receptor subunit alpha 4  
RT cDNA."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF225912; AAF34716.2; -  
KW Receptor  
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Percent Similarity: 60.423 Percent Identity: 42.345

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US-07-938-154-10 x Q9ET51 ..

Align seg 1/1 to: Q9ET51 from: 1 to: 629

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18 LeuLeuLeuLeuGlyThrGlyLeuLeuProAlaSerSerHisIleIleu 34
94 ..... GAGAGCGGCTAGTGAAGCATCTTAGATCCCTCC 130
||||| ||| ::::::::::| ::::::::::|
34 rArgAlaHisAlaGluGluArgLeuLeuLysArgLeuPhe.....SerG 49
131 GCATTAACAAGCTGATTCGTCAGCTACTAAGCGCTCTGAGCTGGTAC 180
||||| ||| ::::::::::| ::::::::::|
49 LTYTyrHisLysTrpSerArgProValAlaHisIleSerAspValIleu 65
181 GTACACCTCATGGTATCATGCTGCTAGCTATTAGTGTGCAGAGCGGGA 230
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66 ValArgPheGlyLeuSerIleAlaGlnLeuIleAspValAspGluLys 82
231 GCAGATCATGACCAACATGTCTGCTGACGAGAGTGGAGATTAAC 280
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82 ngInMetMetThrThrAsnValTrpValLysGlnGluTrpHisAspTyr 99
281 GCCTCATCATGGAAGCTGAGAGCTTGACATATGAAAGTCCGCTC 330
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99 yLeuArgTrpAspProGlyAspTyrGluAsnValThrSerIleArgIle 115
331 CTTTCCAAACATCTGGCTCCGATGTGTTCTTACACAACTGCTGA 380
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116 ProSerGluLeuIleTrpArgProAspIleValLeuTyrAsnAsnAla 132
381 CGCATGTACGAAGTCTCTTATTCATCAATGCTGTGCTCTATGATG 430
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132 pGlyAsnPheAlaValThrHisLeuThrLysAlaHisIleLeuPheTyr 149
431 GGAGCATCTTTGGCTACGACCTGCATATGATGCTGATGCTGATGAT 480
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149 LysArgValGlnTrpHisProProAlaIleLysIleSerSerCysSer 165
481 GAGGTGAACCACTCCATTTGACACGAGAAATTCACCATGAAGTTTG 530
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166 AspValThrPheProPheAspGlnGlnAsnCysThrMetLysPheG 182
531 CTCATGACCTACGACCGCTAGTGAATTCACCTGGTG...CTCAAAAGT 577
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182 ySerTrpTrpTrpAspLysAlaLysIleAspLeuValSerMetHisSer 199
578 ATGTGGCCAGTGTGATGACTTCACACCGAGGAGGAGTGGACATCAT 627
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199 rGValAspIleLeu...AspPheTrpGluSerGlyLysTrpValIleVal 214
628 GCAGTGGCCAGGCGGACGACGAGAAACCAAGAGAC.....TCCAC 668
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215 AspAlaValAlaGlyThrTyrAsnThrArgLysTyrGluCysAlaGlu 231
669 CATATGACATCACCATTGATCATGCTTGCACAAACCATCTTGT 718
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231 eTyrTrpAspIleThrTyrAlaPheIleIleArgArgLeuProLeuPhe 248

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719 ACATATCAACCTCATCATACCCCTGGCTACTATCAACCTGCGGCATC 768
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769 CTGGCTTTTACCTGCCCTCAGACTGTGTGAAGAATGACACTTTGTAT 818
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265 LeuValPheTyrLeuProSerGlyGlyGluValThrLeuCysIle 281
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281 eSerValIleLeuSerLeuThrValPheLeuLeuIleThrGluIleI 298
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919 ACCATGATGTAGTACCTTCTCATGCTGACACGAGGCTGTGTGCTCA 968
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969 TGTGACCAACCGCTGCTTACACGACACACCATGGCCCCGTGCTCAAG 1018
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1019 TGGTCTTCTCGAGAACTGCCACCTGCTCTTCTGCGACGACCA... 1065
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1254 .....CAGCGTCT 1254
476 rSerGlnGluAlaAlaGlySerIleArgCysArgSerArgSerIle 493
1254 ..... 1254
493 lntTyrCysValSerGlnAspGlyAlaAlaSerLeuThrGluSerLys 509
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AC 046133;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE NICOTINIC ACETYLCHOLINE RECEPTOR, ALPHA2 SUBUNIT (FRAGMENT).
GN NACHR.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthoptera; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
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RA Stetzer E., Maelicke A., Thees R., Hermen B.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AJ000391; CAA04053.1; -.
DR InterPro; IPR001175; -.
DR Pfam; PF00065; neur_chan. 1.
DR PRINTS; PR00252; NRIONCHANEL.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
FT NON_TER 1
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5 LysArgLeuTyrAspAspLeu.....SerAsnTyrAsnArgLeuI 19
147 TCGTCCAGCTACTAAGGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTAT 196
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197 CATTTGGCTACGCTCATTAAGTGTGCAGAGCGGAGCAGATCATGACACC 246
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247 AATGCTCTGACGACCCAGCAGAGTGGAGATTAACCGCTTCACATGAGACC 296
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297 TGAGGACTTCGACAAATATGAAAGTCCGGCTCCCTCCAAACATCT 346
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347 GCGTCCAGATGTGGTCTTATACAAACAATGCTGACGGCATGACAGATC 396
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397 TCCCTCATTCGCAATGCTGTGTCTCTCCATATGATGACACATCTTTGGCT 446
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119 sProProAlaIleTyrLysSerSerCysGlnIleAsnValGluTyrPheP 136
497 CATTTGACACGACAGATTTGCACCATGAATTCGCTACATGACCTACGAC 546
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547 CGTACTGAGATGACCTGGTG.....CT 569
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620 ACATCATGACGACGTCCGAGCGCGACGCAACGAG..... 651
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652 ...AACCCAGACGACCTCCACCTATGTGACATCACCTATGACTTCATCAT 698
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699 TCGTCCGAACACCTCTTACACTATCAACCTGATCCCTGCGCTAC 748
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Align seg 1/1 to: 046134 from: 1 to: 540

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227 GCGAGAGATCATGACCAACAATGGTGGTGACCCAGGAGTGGAGAGAT 276
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327 GCTCCCTTCCAAACACATGTGGTCCAGATGTGGTTCTATACAAATG 376
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68 sValProSerGlnHisIleTyrLeuProAspIleValLeuTyrAsnAsnA 85
377 CTGAGCGCATGTACGAGCTGCTCTTATTCGAATGCTGTGCTCTCTAT 426
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427 GATGGCAGCATCTTTGGCTACCACTGCCATCTACAGAGTGCATGCA 476
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285 ervaValValThrIleAlaValLeuAsnValAsnPheArgSerProVal 301

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DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA-3 SUBUNIT.
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN NCBI_TaxId=7102;
RP SEQUENCE FROM N.A.
RA Schulte T., Oelkers N., Adamczewski M.:
RT "Preliminary: Cloning of nicotinic acetylcholine receptor subunits of
RT Heliothis virescens".
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

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DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE NACRBETA-96A PROTEIN.
DE NACR-BETA-96A OR NACRBETA-96A OR CG6798.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
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RP SEQUENCE FROM N.A.
RP STRAIN=BERKELEY.
RC MEDLINE=20196006; PubMed=10731132.
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sultion G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Aaril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spralling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL: AE003748; AAF56304.1; -.
DR Flybase: FBgn0004118; nacr-beta-96A.
DR InterPro: IPR001175; -.
DR Pfam: PF00065; neur_chan.1.
DR PROSITE: PRO0252; NRIONCHANNEL.
DR PROSITE: PS00236; NEUROTRION_CHANNEL.1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ
SEQUENCE 519 AA, 60140 MW, DDE67674529D2FCB CRC64;

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 Ratio: 3.056          Gaps: 10  
 Percent Similarity: 70.495      Percent Identity: 42.772

alignment\_block:

us-07-938-154-10 x 09VC71 ..

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71 uLysAsnGlnValMetThrThrAsnLeuThrValLysGlnArgTrpPheA 88
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325 CGGCTCCCTTCCAAACACATCTGGCTCCAGATGTGTCTTATACAAACA 374
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375 TGCAGAGGCGCATGTACGAAGTCTCTTATTCACATGCTGTGCTCCT 424
121 nTrpAspGlyAsnTrpGluValThrLeuMetThrLysAlaThrLeuLysT 138
425 ATGATGGCAGCATCTTTGGCTACCACTGGCATTCATACAAAGTGCATGCG 474
138 yTrpTrpGlyGluValPheTrpIuProProAlaIleTyrLysSerSerGys 154
475 AACATGTAGGTGAAGCACTTCCATTGACGACAGACAAATTTGCACCATGAA 524
155 GluMetAsnValGluTrpPheProTyrAspIuGlnIleCysPheMetLys 171
525 GTTTGGCTCATGACGACCTACGACCGTACTGAGATGACCTGTGCTCAAAA 574
171 sPheGlySerTrpThrTyrAsnGlyAlaGlnValAspLeuLysHisLeuA 188
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205 PheTyrLeuSerValGluTrpAspIleLeuGlnValProAlaThrLysAs 221
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221 nGluGluTyrTrpProAspThrLeuGluProPheSerAspIleThrPheL 238
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238 yLeuThrMetArgValGlyThrLeuPheThrValAsnLeuIleVal 254
739 CCCTGCTACTCATCACTCGTGGCGCATCTGCTTCTTCACTCGCCCTC 788
255 ProCysValAlaLeuThrPheLeuThrValLeuValPheThrLeuProse 271
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271 rAspSerGlyGluLysValThrLeuCysIleSerIleLeuValSerLeuT 288

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889 GTACCGGTGGGCAAGTACATGTTTACCATGATGCTATCACTT 938
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305 ValProLeuLeuGlyIleLeuLeuPheThrMetIleLeuValSerIe 321
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939 CTCCATCGTCACCAAGCTGTGTGTCTCAATGTGACCAACCGTCCCTA 988
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321 uSerValIlePheThrValCysValLeuAsnIleHisPheArgSerPro 338
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368 .....ProAspTyrAspAspSerThrProSerAsnGlyTyrThr 380
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381 AsnGluIleLeuPheValArgAspSerIleSerAspPheProSerGluPhe 397
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1230 TGCAGCCGCCCGGG..... 1245
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397 sAspSerGlnAspGlyAlaTyrAspAsnGlyMetGlnAsnSerValAsp 414
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1246 .....CGCTGTGGGCGCTGACGAGCTGTGCGCTCCG 1278
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414 erAspAsnValIleProArgAsnLeuThrPro.....GluValLeu 427
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1279 GAGACAGTGTAGGCGCTTACGCTTATTCGAGACATGCGAAGTAGGA 1328
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428 GlnAlaLeuArgAlaValArgPheIleAlaGlnHisIleLeuAspAla 444
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1329 TGATGACCAAGTGTGAGGAGCACTGGAATACGTTGCGATGATG 1378
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444 PlysAspAsnGluIleValGlnAspTyrPlysPheValSerMetValLeu 461
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1379 ACCGCGTGTCTGTGATCTTGTCTTGTCTTGTCTTGTGAGACCTG 1428
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461 spArgPhePheLeuThrPhePheThrLeuSerGlyValPheGlyThrLeu 477
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DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE NICOTINIC ACETYLCHOLINE RECEPTOR DALPHA 4 SUBUNIT PRECURSOR.
GN NACR-ALPHA-80B OR NACRALPHA-80B OR CG12414 OR CG17552.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]

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RP SEQUENCE FROM N.A.
RA Lamsdell S.O., Millar N.S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL: AJ72159; CAB7445.1; -.
DR FlyBase: FBgn0037212; nacr-alpha-80B.
DR InterPro: IPR001175; -.
DR Pfam: PF00065; neur_chan_2.
DR PRINTS: PR00252; NR10CHANNEL.
DR PROSITE: PS00236; NEUOTR_ION_CHANNEL, 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 568 NICOTINIC ACETYLCHOLINE RECEPTOR DALPHA 4
FT SUBUNIT
SQ SEQUENCE 568 AA; 64473 MW; C5C0096F1C6769 CRC64;

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Quality: 1087.50 Length: 527
Ratio: 3.038 Gaps: 9
Percent Similarity: 67.932 Percent Identity: 42.125

alignment_block:
US-07-938-154-10 x Q9NFR5 ..
Align seg 1/1 to: Q9NFR5 from: 1 to: 568

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102 GCTAGTGAGACATCTTAGATCCCTCCCGCTAATAACAAGTGTGTC 151
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43 gleuTyrAspAspLeuLeu.....SerAsnTyrAsnLysLeuValArg 58
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152 CAGCTACATACGCGCTGAGCTGAGTGTGACTGACAGCTCATGCTATCATG 201
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58 roValValAsnThrThrAspValLeuLysValCysIleLeuLysLeu 74
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202 GCTCAGCTCATTAGTGTGACAGCGGAGAGCATCATGACCAACATGT 251
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252 CAGCGTACCCAGAGTGGGAGATTAACCGCTCACATGGAAGCGTGAAG 301
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91 utrPValGlnGlnSerTyrAspTyrLysLeuArgTyrGlnPolySg 108
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 16, 2001, 02:02:36 ; Search time 1190.68 Seconds  
(without alignments)  
12003.825 Million cell updates/sec

Title: US-07-938-154-10

Perfect score: 1512  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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258: em\_gss\_inv56:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	489.2	32.4	932	220	CNS03RNG
3	285.4	18.9	801	147	BF311784
4	258	17.1	755	147	BF311784
5	250	16.5	583	242	AW914206
C 6	247.2	16.3	856	221	AK017571
7	232.4	15.4	192	120	CNS023C0
8	228.6	15.1	854	220	CNS023C0
9	222	14.7	864	107	AL120692
10	214.4	14.2	622	166	BE382752
11	213.8	14.1	627	10	AA673078
12	210.6	13.9	616	145	BF206289
13	210.4	13.9	932	169	BF794373
14	210.2	13.9	754	220	CNS02R28
15	206.2	13.6	809	153	BE404575
16	203.6	13.5	629	140	BE780326
17	201	13.3	1000	140	BE799894
18	197	13.0	306	2	AA101302
19	191.8	12.7	878	147	BF309612
20	179.4	11.9	539	11	AA711800
21	176	11.6	520	22	AL593905
C 22	173.6	11.5	786	221	CNS04J50
23	172.6	11.4	566	9	AA596914
24	171	11.3	947	221	CNS0303J
25	169.4	11.2	479	10	AA636687
26	167.8	11.1	514	10	AA688727
27	167.6	11.1	1052	106	AL530299
28	165.4	10.9	497	10	AA636794
29	165	10.9	476	9	AA616513
30	163	10.8	915	150	BF569238
31	160.4	10.6	839	220	CNS0296F
32	158.2	10.5	946	11	AA755688
33	156.2	10.3	1011	105	AL514484
34	155.8	10.3	429	149	BF471300
35	154.8	10.2	660	147	BF307986
36	154.8	10.2	806	147	BF305214
37	154.2	10.2	433	13	AA793919
38	152.6	10.1	597	173	BF080409
39	152.4	10.1	713	147	BF309251
40	151.6	10.0	554	138	BE664308
41	150.8	10.0	1835	192	AK010496
42	149.6	9.9	438	150	BF544638
43	147.6	9.8	660	10	AA637462
44	146.8	9.7	982	221	CNS03F40
45	145.6	9.6	960	147	BF310272

## ALIGNMENTS

RESULT 1  
LOCUS CNS03RNG/c  
DEFINITION Tetraodon nigroviridis genome survey sequence T7  
050604 of library 6 from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION AL257677.1  
VERSION AL257677.1  
KEYWORDS GSS: genome survey sequence.  
SOURCE Tetraodon nigroviridis.  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 1001)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fitzames,C., Fisher,C.,

REFERENCE JOURNAL AUTHORS  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
2 (bases 1 to 1001)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Bonneau,L., Fisher,C., Bernot,A., Fitzames,C., Wincker,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 1001)  
REFERENCE JOURNAL AUTHORS  
Direct Submission  
Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases  
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetraodon.  
FEATURES  
source location/Qualifiers  
1..1001  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone\_lib="cg"  
/note="Genoscope sequence ID : COB050BD02LPI-end : T7"  
BASE COUNT 245 a 268 c 308 g 175 t 5 others  
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Best local similarity 78.5%; Pred. No. 6.9e-119;  
Matches 609; Conservative 1; Mismatches 164; Indels 2; Gaps 2;  
357 TGTGTTCTATACAACTGCTGACGATGACGATGCTCTTCTATTCATGCTGT 416  
1 111 111 111 111 111 111 111 111 111 111 111 111 111 111  
DB 818 TTTGG 759  
417 GGTCTCTATGATGACGATCTTTGCTACCACTGCTACCTCAAGAGTGCATGCA 476  
111 111 111 111 111 111 111 111 111 111 111 111 111 111  
DB 758 GGTCTCTACGACGACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699  
477 GATGAGGGAAGGACTTCCGATTTGACGACGAGAAATGACCAATGAGTGGCTAT 536  
111 111 111 111 111 111 111 111 111 111 111 111 111 111  
DB 698 GATGAGGGAAGGACTTCCGATTTGACGACGAGAAATGACCAATGAGTGGCTAT 639  
537 GACCTACGACGCTACTGATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCT 596  
111 111 111 111 111 111 111 111 111 111 111 111 111 111  
DB 638 GACCTACGACGCTACTGATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCT 579  
597 CTTCACACCCAGCGGGGAGTGGGACATCATGCACTGCCAGGCCGACGACGAC 656  
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657 AGACGACCTCAGCTATGATGACATCAGCTATGATGATGATGATGATGATGAT 716  
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DB 518 GGGCGAC -CCACTACGATGACATCAGCTATGATGATGATGATGATGATGAT 460  
717 CTACACTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 776  
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DB 459 TTACACTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400  
777 CTACCTGCGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836  
111 111 111 111 111 111 111 111 111 111 111 111 111 111  
DB 399 CTACCTGCGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340  
837 CACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895  
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DB 339 CACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 280  
896 TGTGCGGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955  
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Df	279	TGGGAGGGAAGTATCGATGTTCACCATGCTGCCTGGTCACTTCCTGCATCGTACAGAGC	220		
OY	956	TGTTGATGTCATATGTGACACACCCGCTGCCCTTACCACGACACCATGATGGCCCCGGGGTCA	1015		
Df	219	TGTGCGTGTCATATGTGACACACCCGCTGCCCTCACGACACCATGATGCCCGTGGGGTCA	160		
OY	1016	AGGTCGCTTCCTGAGAAAGCTGCCCACCCGCTTCCTTCCTGACACGACGACGACGCT	1075		
Df	159	AATATGCTTTCCTGCABAMACTTCGGGGCTTCTCTTTATGCGCCAGCCAGAACAGct	100		
OY	1076	GTCACGTCACAGCTCTGCGCTTAGAGAGCGCCACGACGACGCTGAGGGCGAGGCG	1131		
Df	99	GCGAGCCGACAGCGCTCCGTCAGCGCGCGGCGTCAGAGAACAAGAGGGGAGG	44		
RESULT 2	CNS0ZDCP	932 bp	DNA	GSS	13-MAY-2000
LOCUS	DEFINITION	Tetraodon nigroviridis genome survey sequence PUC-ori end of clone 260G11 of library G from Tetraodon nigroviridis, genomic survey sequence.			
ACCESSION	VERSION	AL192274.1	GI:7830378		
SOURCE	KEYWORDS	GSS: genome survey sequence.			
ORGANISM	Tetraodon nigroviridis.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.				
REFERENCE	1 (bases 1 to 932)				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bounneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.				
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 932)				
AUTHORS	Roest-Crollius,H., Jallion,O., Dasilva,C., Bounneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.				
JOURNAL	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence				
COMMENT	Unpublished				
FEATURES	Genoscope.				
SOURCE	Direct Submission				
COMMENT	Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.				
LOCATION	Qualifiers				
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ORIGIN	/clone="260G11"				
ORIGIN	/clone="lib-g"				
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ORIGIN	PUC-ori"				
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Matches 577; Conservative 9; Mismatches 137; Indels 1; Gaps 1;	Matches 577; Conservative 9; Mismatches 137; Indels 1; Gaps 1;				
OY	344	TCGAGCTCCCAATGATGCTTATACACATGCGAGCGATCATAGAGTCTCTCT	403		
Df	192	TTTTCTCTTCTTCTTGGGCGGCGCCACAGCTGACGGGGTATACAGATCTCT	251		
OY	404	ATTCCAAATGCTGTGCTCTCTTATGATGCGAGCATTTTGGCTACCACTGCATCTACA	463		

D	b	252	ACTCTCAAGCGGGGTGTCWCMVCMGACGGCACATATATCMTGCGCTCCACGACATCTTACA	311
O	y	464	AGAGTCAGTSCAAGATTGAGTGGAAGCACTTCCCATTTTGACCAGCAAGATTGCACATAGA	523
D	b	312	AAMCGCGTGTATGAAGAAGGAGGAAGCATTTTMCCTTCGACAGCAAGAACTGCACCTCG	371
O	y	524	AGTTTGGCTCATGAGAACCTACGACCGCTATGTGATGTGACCTGGTGGCTCAAAAATGTATGG	583
D	b	372	GCTTTCGCTCTGAGACCTACGACCGCACCGGAGCAGMCTGGCTCTCCGCCGACATGG	431
O	y	584	CCAGTCTGGATGTACTTCAACACCAGCGGGGAGTGGGACATATCGCATCGACCGCAC	643
D	b	432	CCAGCATGATGATCTTCAACCCCAAGTGGGAGTGGACATATCGCTCCGCGGACAG	491
O	y	644	GCAACGGAACCCAGACGACCTCCATATGTGGACATCACACTTATGTACTTATCGTGC	703
D	b	492	GGAACGGAACCCCGGGGACCCGACCTTACGTGACATCAGTACGAMTTTCATCATCCG-C	550
O	y	704	GCAACCACTCTTCAACCACTATGAACTCATATCCCGCGGACATCACTACCTGGCG	763
D	b	551	AGAACTCTTTTWTATACATCAATCATATCATATCCGTCGATCATCACTCTCG	610
O	y	764	CAATCTGGTCTTCTTACCTGCCCTCAGACTGTGTGTAAGATAATGACATCTGTATTCTG	823
D	b	611	CATCTCGGTCTTCTTACCTGGCCGCTCCAGCTCGGCGAAGATGACGCTGATCTCTCG	670
O	y	824	TGCTGTACACTCAACCGGTGTCTCTGCTCATCTTCCATATGTGCTCCACCTGCC	883
D	b	671	TGCTGTGCGCTTCAACCGCTTCTCTGCTGATATTCCAAATATGCTCCGCTCACCTTGC	730
O	y	884	TGCATCTACCGCTGTGTGGGCAAGTACCTCATATGTTTTACATATGTTGATGACCTTCTCA	943
D	b	731	TGATGATCACTTTGGTGGGGAAGTGTGATGATTCACATATGTTCTGGTACACTTCTCA	790
O	y	944	TGCTGACCAAGCGGTGTGTGCTCATATGTGACACACCGCTGCTTACACGACACATGG	1003
D	b	791	TGCTGACGAGCGTGTGCGCTCATATGTGACACACCGCTGCTCCACACACACATGC	850
O	y	1004	CCCCCGGGTCGAAGGTGCTTCCGTGGGAAGCTGCCCAACCTGGCTTCCGTGGACGACG	1063
D	b	851	CCCCGGGGTCAAAATGTGTCTTCTCCAGAAGCTCCGCGTTCCTTCATGCGCCACG	910
O	y	1064	CACG 1067	
D	b	911	CAGC 914	
R	E	S		
R	E	S		
L	O	C		
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I	N	F	60189728BFL NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126725 5'	
D	E	F	mRNA sequence.	
A	C	C	BF311784	
K	E	S	BF311784.1 GI:11259546	
E	S	T	EST.	
K	E	S	human.	
S	O	U	Homo sapiens	
O	R	G	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
M	A	J	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
R	E	F	NIH-MGC http://mgc.nci.nih.gov/	
T	I	T	1 (bases 1 to 801)	
J	O	R	Unpublished (1999)	
N	A	M	National Institutes of Health, Mammalian Gene Collection (MGC)	
C	O	M	Contact: Robert Strausberg, Ph.D.	
			Email: rgs@db.riken.jp	
			Tissue Procurement: ATCC	
			cDNA Library Preparation: Ling Hong/Rubin Laboratory	
			DNA Sequencing by: Incyte Genomics, Inc.	
			Clone distribution: MGC clone distribution information can be	
			found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov	
			Plate: L10M016 row: p column: 22	



QY	632	TGCCAGGCGCAGCAACGAGAAACCACAGCACTCC-----ACCTATGTGGACATCA	862
Db	498	CCCCGGGCTACAAMCATGAATATCAAGTACAACTCTGTGAGAGATTTACCAAGACATCA	557
QY	683	CCTATGACTTATATATTGTCGCAAACCACTCTTTAAGTAATCAACCTGATGCCT	742
Db	558	CGTACTGGCTGTACATCCGTGCGCTGCGCGGTCTTCAACATATAACCTCATATCCCT	617
QY	743	GCGTACTCATCACTCGCTGGCCATCCTGGTCMTTACGCGCCTCAGACTGTGGTAAA	802
Db	618	GCGTCTCATCTCTTCTCTCACTGTGTTGTCTTACAGCCCTCCGATGTGGGAGA	677
QY	803	AGATGACATTTGTAATTTCTGTGCTGTAGACACACAGGTGTTCTGCTGCTATCTCCA	862
Db	678	AAGTAGACACTCTGCATCTCTGTGCTCTCTTCCCTGAACTGTCTTCTCTGTATCACCG	757
QY	863	AGATGTGCCCACCACT	880
Db	738	AGACCAATTCCTTTCACCT	755

RESULT		5							
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DEFINITION	AZ384944	583 bp	DNA	GSS		02-OCT-2000			
ACCESSION	F01013L1F	Mouse 10kb plasmid	UUGC1M library	Mus musculus genomic clone UUGC1M0143L1 F,	DNA sequence.				
VERSION	AZ384944								
KEYWORDS	AZ384944.1	GI:10498644							
SOURCE	GSS.								
ORGANISM	house mouse.								
	Mus musculus								

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
(Phase 1 to 583)	Duno, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0143 row: L column: 11  
Seq primer: CCGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 563.  
Location/Qualifiers  
1. .583

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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 kb

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMPD2 (g14732114[9b]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	16.5%	Score 250;	DB 242;	length 583;
Best Local Similarity	65.8%;	Pred. No. 2e-55;		
Matches 383;	Conservative	0;	Mismatches 190;	Indels 9;
				Gaps 1;

QY 484 GGGAGGACGCTCCCATTTTGGACGACACAAATTTGACCCATGTGAAGTTTGGCTCATGAGACCTAC 543

Db 1 GTGACCTACTCCCGTGTGACTACCAAACTGGACCATGAAAGTTGGGCTCCTGGTCTAC 60

QY 544 GACCGTCTAGATTGACCTGCTGCTCTAAAAAGTAGTGGCCAGCTGTGATCTTCACA 603

Db 61 GACAGGCAAGCAATCGACCTGGTCTCATTTGGTCTCCATCATGAACCTCAAGACTATTGG 120

QY 604 CCGAGGGGGAGTGGGGACATATCGCACTCCGACGCGGAGCGACCAAGGAAAGCCAGAGAC 603

Db 121 GAAAGTGGGAGTGGGGCATCATTTAAAGCCCCGGGCTCAAAACATGAAATCAAGTACAC 180

QY 664 TCC-----ACCTTGTGGACATACCTTATGACTTCATCTATGTGGTCCAAACACATC 714

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QY 715 TTCTACACTATCAACCTCATCATCCCTGGCTACTGCTATCACTCGGTGGGCACTCTGTC 774

Db 241 TTCTACACATCAACCTCATCATTCGGTGGCTGCTCATCTCTCTCACTGTGCTCTGTC 300

QY 775 TTCTACCTGCTTCAGACTGTGGTGAAGATGACACTTTGATTTTCTGTGCTGTAGCA 834

Db 301 TTCTACCTGCTTCAGACTGTGGGGAAGGTGACCTGTGATCTCCGTCCTCTCC 360

QY 835 CTGACGGTGTCTCGTGGCATCTCCAAAGATGTGCTCCCACTCCCTCCATGTACGG 884

Db 361 CTGACGGTCTTCTCGTGGATCCCGGAGAACATCTCTTCCACCTCATGTGATCCCTCC 420

QY 895 CTGTGGGGCAAGTACCTCATGTTTACCATGTGCTAGTACCTCTTCCATTCGCATCAGC 954

Db 421 TTGATGGGGAGTACTCCTCTTCACATATGATTTTGTCACTTGTTCATTCGTCATCACA 480

QY 955 GTGTGTGTGCTCAATGTGCACCAACCGCTGCGCTTACCAGCAGACCAATGTGACCCCTGGTCT 1014

Db 481 GTCTTGTGCTCAAGCTGACATCAGAAAGTCGAGACCAACAGATGTGCCAATTGGGTC 540

QY 1015 AAGGTGTCTCTCTGAGAAAGCTGCCACCTGCTCTTCTCTG 1056

Db 541 AAGGCTGTGTTTTGAACCTTCTCCCGAGGGTCATGTTATG 582

RESULT	6
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LOCUS	CNS04DRH 856 bp DNA
DEFINITION	Tetradon nigroviridis genome survey sequence pUC-Orig of clone 103M19 of library G from Tetradon nigroviridis, genomic survey sequence.
ACCESSION	AL286118
VERSION	AL286118.1 GI:8024562
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetradon nigroviridis.
ORGANISM	Tetradon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphia; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodonidae; Tetraodon.

REFERENCE		1 (bases 1 to 856)	Jailion,O., Dasilva,C., Fizames,C., Fisher,C., Roest-Crollius,H., Billaud,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J.
AUTHORS			
TITLE			Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 856)	Roest-Crollius,H., Jailion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brotier,P., Quetier,F., Saurin,W. and Weissbach,J.
AUTHORS			
TITLE			Human gene number estimate provided by genome wide analysis using tetraodon nigroviridis DNA sequence
JOURNAL		Unpublished	
REFERENCE		3 (bases 1 to 856)	Genoscope.
AUTHORS			
TITLE			Direct Submission
JOURNAL		Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases	
COMMENT		This sequence is a single read and was generated as part of a large scale clone end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.	
FEATURES			
source		1. 856 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone_1lb="G" /clone_1lb="G" /note="Genoscope sequence ID : C0BGI03AGI0SP1-end : PUC-Ori"	
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Db	696	CAGTGCTCAGCGAGGTTCGAGGGCTCCCGATGACCAGAAGCATGTAAAGTAGACGG 637	
OY	432	CAGATCTTTTGGGTACCACTGCTCAAGAGAGCATGCAAGATTGAGGTGAAGA 491	
Db	636	CGCATCACCTCGAGAGCGCTCCCGCAGACTCAAAATCTGCTCGACCATGAGCTACTT 577	
OY	492	CTTCCCATTTGACACGACAATTTGACCAATGAAGTTTGCTCTATGACCTACGACCGTAC 551	TITLE
Db	576	CTTCCCCTTCGACGAGGACGACACTGACCAAGAGTTGCGTCTCTGAAGTTACGACGCGAC 517	JOURNAL MEDLINE REFERENCE AUTHORS
OY	552	TGAGATTGACCTGTGTCTCAAAGTGTTGGCAGCTGTGATGATTCACACCCGACGG 612	
Db	516	CATGTTGACCTGATCTGTATGCCAAAAGCAGGTGATGCCAATACTTCTTCMAAACGG 457	
OY	612	GGAATGGGACATCATGCGCACTGCCAGCGG---ACGACAGAGACCCAGAGACTCCAC 668	TITLE JOURNAL REFERENCE AUTHORS
Db	456	CGAGTGGGAGATCTTAAGTGMACCRNRTAAAGGAAACCGGAGAGCGCCCTGNACNC 397	
OY	669	CTATGTGACATCATGACTATGCTGATCTGTCGCAACCACTCTCTACACTATVCA 728	
Db	396	GTACCCCTTCACTACGATATCTTCACTCCCGGAGGCGGCTCCGCTGTCTMAACCTCTT 337	
OY	729	CTTCAATCATCCCTGCGCTACTCATCATCTGCTGCGCCATCTTGTCTTACTGCCCCC 788	
Db	336	CTCTATCATCCCTGCTTGGTCTATCTCTCTACCTCTACGCTGCTGTCTTCACTCCCTC 277	
OY	789	AGAGCTGTGAAAAAGATGACATTTGATTTGCTCTCTCTAGCACTACCGGTGTTCC 848	
Db	276	AGACGAGAGAAAAAGTTGTCTCTCTCCACCTCTGATGATACCGGTGTTCCCT 217	
OY	849	GCTGCTCATTTCCAAGATTTGCTCCCACTCCCTCGATGATACCGGTGTTCCCT 908	
Db	216	CCTGCTCATTAAGAAATTCATCCCTCTCTCTCCCAAGTATCCCTCATTCGCGAGGA 157	
OY	909	CCTCATTTTACATGTTGCTGCTATCAC-CTTCTCCATCTCTACACAGCGTGTGCTCA 967	
Db	156	CTTCTCTTATCATATATATATGATGCTCTCTCATCATGCTACCGCTTCTGTCATCN 97	
OY	968	ATGTCACACACCG---CTCGCTACACAGCAGCAGCAATGAGCCCTGGGTCAAGTGGTCT 1024	
Db	96	ACGTGACACACCGCTCTCGGCACTACACACCCCTTGTCTCTTGGTGGCAACTCTCT 37	
OY	1025	TTCGCGAAGATGCGCCACCTGCTCTCTCTGAG 1059	
Db	36	TCTGTGAGAAGCTTCCCAAGCTGCTCTGATGCGG 2	
RESULT	7		
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DEFINITION	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730417K16, full insert sequence.		
ACCESSION	AKO1571		
VERSION	AKO1571.1 GI:12856874		
KEYWORDS	cap trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) 8 days embryo cDNA to mRNA, clone_1lb:RIKEN full-length enriched mouse cDNA library clone:5730417K16.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (sites) Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning Methods Enzymol. 303, 19-44 (1999)		
JOURNAL	2 (sites) Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
REFERENCE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS	3 (sites) Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kikuno.H., Ishii.Y., Nakamura,S., Hazama.M., Nishino.T., Harada.A., Yamamoto.R., Matsumoto.H., Sakaguchi.S., Ikegami.T., Kashiwagi.K., Fujiwara,S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E., Matsuhira,M., Yoneda,T., Ishikawa,T., Ozawa.K., Tanaka.T., Matsuda,S., Okazaki,Y., Muramatsu,M., Inoue.Y. and Hayashizaki,Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
REFERENCE	4 (sites) The Riken Genome Exploration Research Group Phase II Team and PANTOM Consortium.		
AUTHORS	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)		
TITLE	5 (bases 1 to 2257)		
JOURNAL	Adachi,U., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukuishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu.N., Hiramoto.K., Hiroake.T., Horii.F., Imotani.K., Ishii.Y., Itoh.M., Izawa.M., Kato.H., Kawaji.J., Kojima.Y., Kono.H., Kouda.M., Koya.S., Kurihara.C., Matsuyama.T., Miyazaki,A., Nishi.K., Nomura,K., Numazaki,R., Oho,M., Okazaki,Y., Okido,T., Owa.C., Saito.H., Saito.R., Sakai.C., Sakai.K., Sano.H., Sasaki,D., Shibata,K., Shibata,Y., Shigaawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa.A., Takahashi.F., Tanaka.T., Tejima.Y., Toya.T., Yamamura.T., Yasunishi.A., Yoshida.K., Yoshino.M., Muramatsu.M. and Hayashizaki,Y.		
REFERENCE	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,		









BASE COUNT	137 a	189 c	144 g	157 t	rapidly, forming contractile myotubes and producing characteristic muscle proteins.
ORIGIN					"

Query Match	14.1%	Score	213.8	DB	10	Length	627
Best Local Similarity	63.7%	Pred. No.	8e+46				
Matches	347	Conservative	0	Mismatches	187	Indels	11
						Gaps	1

QY	513	TTGACCATGAATTTTCGTCATGAGACCTGACACCGTACGTGAGTATGAGTATGACCTGCTGCTAA	572
Db	12	TGCGAGCATGAACTGGGACCTGGACCTGACCTATGACGCGCTCTTGGGGGGCGCATTTAACCCGGA	71
QY	573	AAGTGAATGGGCAAGTCTGGATGATGACTTCACCCACGCGGGAGTGGGACATCATGCGACT	632
Db	72	AATGTACACGCCGACCTTAGTAACTTCAATGAGAGACGGGAGTGGGTGATCAAGGAAGC	131
QY	633	GCCAGCGCCAGCGAACGAGAACCCAGA-----GACTCCACCTATGTGGACATC	681
Db	132	TGCGGGCTGGAACTACGGGTGTTCTATCTGCTGCGCCACACATCCCTACCTGGACATC	191
QY	682	ACCTATGACTTATCATTTGGTGGCAACACACTCTTCTACATATTAACCTATCATCC	741
Db	192	ACCTACCACTTCTCTCATGAGGCGGCTGCGCCCTCTACTTCAATGTCAACGTCATATTC	251
QY	742	TGCGTCACTATCACTCGGTGGCGAATCCGGGCTTCCTACGTCGCCCTGACGTCGGTGA	801
Db	252	TGCGTGTCTTCTCCTCTTTTAAACCAAGCTGGTGTCTTACCTGCCACAGACTCAAGGAG	311
QY	802	AAGATGACACTTTGATTTTCTGTGCTGCTAGACACACAGGTTTCTGCTCATCTCC	861
Db	312	AAGATGACCGTGGACACTCTGTCTACTAGTCCGACCGTTCCTCTGTGATTTG	371
QY	862	AAGATGTGGCTGCCACCCCTCCCTCATGTACAGCGTGGGGGGAATACCTATGTTTAC	921
Db	372	GAACTAATCCCTTCCACCTCCACGCGGTGGCCCGATCGGGAAATATATGTGTTTACC	431
QY	922	ATGGTACTAGTACACTTTCATGCTGACACACAGCGTGTGCTCAATGTACACACCGC	981
Db	432	ATGGTCTTTGTATTTGGCGTCAATCATCAACACCTGATCTGTATATACACACACACCGT	491
QY	982	TGCGCTAACACGACACCATGAGCCCTCGGTGATCAAGTGGTCTTCTGAGAAAGCTGCC	1041
Db	492	TGCGCCAGCACCCACATCATGCCCCGAGTGGTGGGAAAGTTTATGAGACATATGCA	551
QY	1042	ACCCCT 1046	
Db	552	AACAT 556	

RESULT	12				
LOCUS	Bf206269				
DEFINITION	Bf206269	616 bp	mRNA	EST	06-NOV-2000
ACCESSION	U01869	22261	NIH_MGC_19	Homo sapiens	CDNA clone IMAGE:4097956
VERSION	Bf206269				
KEYWORDS	Bf206269.1				
SOURCE	EST.				
	human.				

REFERENCE	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 616)	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Contact: Robert Strausberg, ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: ILCM964 row: c column: 21  
 High quality sequence stop: 616.

FEATURES	Location/Qualifiers
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/clone="IMAGE:407996"
/clone_1lb="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

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	Query Match Best Local Similarity	13.9%	Score 210.6	DB 145	Length 616
	Matches 307	Conservative 0	Mismatches 129	Indels 9	Gaps
QY	607	.AGCGGGAGGTGGGACATCATGCGACTGCCGAGGCGAGCGCAACGAGAACCCAGACGACTCC	666		
Db	30	AGCGCGAGGTGGGGCCATCATCAACCCCGAGGCTCAAAACAGGACATCAAGTAACAATCC	89		
QY	667	-----ACCATGTGGACATCACTATGACTATCATATTCGTGGCAAAACCATCTTC	717		
Db	90	TGCGAGGAGATTTACCCCGACATCATACATACGTGCTGTACATCCGGCGCTGCGCTTGTTC	149		
QY	718	TACACTATCAACCTCATCATCCCTGGGCTACTCATCACTCACCCTGCGTGGCAATCCGTCTTC	777		
Db	150	TACACATCAACCTCATCATCCCTGGCGCTGCATCTCTTCCATCACTGTGCTGCTTC	209		
QY	778	TACCGGCCCTGAGATGATGGTGAAGAAAGATGACACTTTGATTTCTGTGCTGTACACAC	837		
Db	210	TACCTGCCCTCCGAGTGGGTGAGGAGGACCCGTGTGATTTCTGTCTCTCTTC	269		
QY	838	ACGGGTTCCTGCTGCTCATCTCCAAGATTGTGCTCCACCTCCCTCGATGTACCGGTG	897		
Db	270	ACGGGTTCCTGCTGCTGATCACTGAGACATCCCTTCACCTCGCTGGTCAATCCCGCG	329		
QY	898	GTCGGCAGTACCTCATGTTTACCATGGTGTGCTAGTCACCTTCTCCATGTGTACCAAGCGTG	957		
Db	330	ATTGGAGATGCTCTCTGTTCACCAATGATTTTGTACCTGTGTCATGTGTCATCCGCTG	389		
QY	958	TGTGTGTCATATGTGACACACCGCTCGCGCTACCAAGCAACCACTGAGCCCTCGGTCACG	1017		
Db	390	TTTGTGTCATACGTGCTACAGAACCCCGAGACACACACATGCTCCCTCATGGGTGAAG	449		
QY	1018	GTGCTTCCTCGTGGAGAACTGGCCA	1042		
Db	450	ACTGATTTCTTGAACCTGCTCCCA	474		

RESULT		13				
Bf794323						
LOCUS	Bf794323	932 bp	mRNA	EST	12-JAN-2001	
DEFINITION	G02253335F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4338600 5' , mRNA sequence.					
ACCESSION	Bf794323					
VERSION	Bf794323.1	GI:12099377				
KEYWORDS	EST .					
SOURCE	human.					

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.



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Db      388  ACACAGAGGCGAGATGAGCTGGTGTGATCGGCTCCACCATGACCTGAGGACTTCT
QY      602  CACCCAGCGGGAGTGAGCATCATGCACTGCCAGGCCAGCGAACGAGACCCAGAGC 661
Db      448  GGGAGACCGGCGATGTTGGTATGATGACGCCCGGGATGACAAACAGACATCAAGTACA 507
QY      662  ACACCC-----ACCTATGTGACATCATCATATGACTTCATCATCTTCGCGCAACAC 712
Db      508  ACTGCTGCGAGAAATCATACGAGCATCATCTTGTGTGATCATCGCGCGCTGCGCG 567
QY      713  TCTTCTACATATCAACCTCATCATCCCTGCGTACTCATCATCCCTGCGCATCTGG 772
Db      568  TCTTCTACATATCAACCTCATCATCCCTGCGTACTCATCATCCCTGCGCATCTGG 627
QY      773  TCTTCTACATATCAACCTCATCATCCCTGCGTACTCATCATCCCTGCGCATCTGG 832
Db      628  TCTTCTACATATCAACCTCATCATCCCTGCGTACTCATCATCCCTGCGCATCTGG 687
QY      833  CACTCAGAGGTGCTCTGCTCATCTCATCAAGATTTGCTCCACCTCCCTGCGCATCTAG 892
Db      688  CTTTACAGGCTTCTTCTTGTGTATCATCAGAGACCATCCGCTGCGCATCTAG 747
QY      893  CGCTGCT 899
Db      748  CCCTGAT 754

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## RESULT 15

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Bg404575      809 bp      mRNA      EST      12-MAR-2001
LOCUS      602420721F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4527821 5',
DEFINITION      mRNA sequence.
ACCESSION      Bg404575
VERSION      Bg404575.1 GI:13298023
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 809)

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REFERENCE      NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: The Cepko Laboratory

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.liml.gov
Plate: LLAM10437 row: 1 column: 06

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High quality sequence stop: 784.

## FEATURES

Location/Qualifiers

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1..809
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/clone="IMAGE:4527821"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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BASE COUNT      197 a      213 c      181 g      218 t
ORIGIN

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Query Match

13.6%; Score 206.2; DB 153; Length 809;

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Best Local Similarity 58.4%; Pred. No. 8.8e-44;
Matches 420; Conservative 0; Mismatches 288; Indels 11; Gaps 3;
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Db      93  CTCATCTAACACCGCTTCATCGCGCGGGTGGAGAAATGTCGATCCGATCCGATGAGT 152
QY      188  TCATGATATCATTTGGCTCAGCTCATTTAGTGTGACAGAGCGGAGACATCATGACACCA 247
Db      153  TTGATATGGCAATACAGCACTTGCGCAATGTGATGAAGTCAACCAATTTATGAGAGAC 212
QY      248  ATGCTGCTGACCCAGAGAGGAGATTAACCGCTTCATCATGAGAGAGAGAGAGAGAGT 307
Db      213  ATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 271
QY      308  ACAATATGAGAGAAAGTCCGCTCCCTTCCAAACATCTGCTCCAGATGTGTTCTAT 367
Db      272  ATGCGATCGAGACACTTCGATTCACAGACAAACATCTGGAAGCTGACATCTGTTCTGT 331
QY      368  ACAACATGCTGAGAGGAGATGAGAGAGTTCCTTCTATTCATGCTGTGCTGCTGCTATG 427
Db      332  ATTAACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391
QY      428  ATGCGAGATCTTTTGGCTACACCTGCTCCATCTACAAAGATGATGCAATGAGTGA 487
Db      392  ACGGTGATTAACCTGAGACCCAGCAGCTTCAAGTGAAGCAAGCAAGCTTTCTCAAGTATG 391
QY      488  AGCATTCCTCCATTTGACAGAGAGATTCACCATGAAATTTGCTGCTCATGAGACCTAC 547
Db      452  CTTCTTCCCTTTGAGACATCAAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 511
QY      548  GTACTGAGATTAACCTGCTGCTCAAAAGTATGAGGAGTCTGCTGCTGCTGCTGCTGCT 607
Db      512  AGCAGAAATGAGACCTTCTCATTTGCTGCTTAAGTATGAGATGAGAGACTTTGGGAAA 571
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Db      572  ACAGTGAATGGGAAATGTCTGAGCGCTGCTGCTTAAGCATGACATCAAGTACACTCTCT 631
QY      667  -----ACCTATGTGAGCATCACTATGATGATGATGATGATGATGATGATGATGATG 718
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QY      719  ACATATCAACCTCATCTATCCCTGCGTACTCATCATCCTGCGCATCTGCTGCTGCTTCT 778
Db      692  ACACATCAAACTCATCATCTATCCCTGCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 750
QY      779  ACCGCGCTCAGACTGTGCTGAGAAAGATGACATTTGATTTTCTGCTGCTGCTGCTGCT 837
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Search completed: October 16, 2001, 03:24:37  
Job time: 4921 sec

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